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## ALIGNMENTS

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KEYWORDS
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FEATURES
BASE COUNT
ORIGIN
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AR012692
LOCUS
                              source
                                                                                                      Unknown
                                                                                                                                      AR012692 1188 bp
Sequence 2 from patent US 5763589.
AR012692.1 GI:3971010
                                       Human membrane protein
Patent: US 5763589-A 2 09-JUN-1998;
Location/Qualifiers
                                                                     1 (bases 1 to 1188)
Hillman, J.L. and Goli, S.K.
                                                                                             Unclassified
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          268
        /organism="unknown"
316 c 362 g
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Ouery Match 99.6%; Score 1183; DB 6; Best Local Similarity , 100.0%; Pred. No. 8.9e-271;

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            ACCAAAGCCCCAGTGCCAGGGACTCCAGACTCACTCTCCAGTGGGAGCAGCAGAGATGTC
                                                  GGGAAGAANCAGGCCCAGATCCTGGCCTCCGAAGCAGAAAAGGCTGAACAGATAAATCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (25-SEP-1999) Pathology, Street, New Haven, CT 06510, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wang,Y. and Morrow,J.S. Identification and characterization of human homologue of stomatin (band 7.2b) present in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 1303)
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Homo sapiens
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                315
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391
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217
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Title: Perfect score:

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AX193464 Sequence
AX261777 Sequence
AX302706 Sequence
AX20095 Sequence
AC026501 Homo sapi
AC004472 Homo sapi
AL53795 Human DNA
AL591668 Homo sapi
AX261093 Sequence
A74641 Sequence 32
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124241 Sorangium C
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Hillman, J.L. and Goli, S.K.
Human membrane protein
Patent: US 5763589-A 2 09-JUN-1998;
Location/Qualifiers
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AR012692
AR012692.1 GI:3971010
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AUTHORS
TITLE
JOURNAL
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13110.468 Million cell updates/sec
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1 GGCTTCTGGGAGCNACCGCT......GGAAGCAGATTTTCCTGATT 1188
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Copyright (c) 1993 - 2000 Compugen Ltd.
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	CAGGGTACAGATGCAAGTNTTGATG	TGGGCTTNGCCAGGAGTCTGGGGA 		Homo sapiens, stomatin- complete cds. BC003025 BC003025.1 GI:12804332	MGC. human. Homo sapiens Eukaryota: Metazoa; Cho	Mammalia; Eutheria; Pri 1 (bases 1 to 1257) Strausberg,R. Direct Submission	Submitted (06-FEB-2001) Gene Collection (MGC), Institute, 31 Center Dr USA	NIH-MGC Project URL: ht Contact: MGC help desk Email: cgapbs-r@mail.ni Tissue Procurement: DCT	CDNA Library Preparatio CDNA Library Arrayed by DNA Sequencing by: Geno BC Cancer Agency, Vanco	Info@bcgsc.bc.ca Steven Jones, Jennifer Susanna Chan, Readman C Letticia Hsiao, Martin	Sen Lee, Victor Ling, C Ness, Pawan Pandoh, Ann Schein, Duane Smailus, Michael Thorne, Miranad	George Yang, Scott Zuyd Clone distribution: MGC through the I.M.A.G.E.	Series: IKAL Plate: 9 K This clone was selected passed the following se Location/Quali	/organism="Hom /db_xref="Locu /db_xref="Locu /db_xref="taxo	/clone="MGC:41 /tissue_type=" /clone_lib="NI /lab_host="DHI	/note="Vector: 23 1093 /codon_start=1 /product="stom	/protein_id="A /db_xref="GI:1 /translation=" EAWVERMGREHRI	GVLYLKIMDYKAS INQAAGWGIRCLR EGKKQAQILASEAE TVAEQYVSAFSKLA
	1081	0y 1141 1 Db 1141 1	RESULT 2 BC003025 LOCUS	DEFINITION ACCESSION VERSION	KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE	JOURNAL	REMARK COMMENT					S	source		CDS		
3ps 0;	09	120 120	180	240	300	360 360	420	480	540 540	009	099	720	780	840 840	006	096 096	1020	1080
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0; Indel	TCCGGAGGTCG(                TCCGGAGGTCG(	CTTTTGCTGAGG	TGCCCCGAAAC/                  TGCCCCGAAAC/	ATGGGCCGATTC(                 ATGGGCCGATTC(	GGATCCGATAT( 	TGACTCTCGAC	CTTACAAGGCA!	CAACCATGAGA:                  CAACCATGAGA:	CCCTGAATGCC/ 	GCCTNCGTTATO	NTGCAGGTGGAGG 	AGTCGGCCATC	AAAAGGCTGAA( 	AGGCTAAAGCT(                AGGCTAAAGCT(	CAGCAGCTTCA(                 CAGCAGCTTCA(	ACTCCAACACT/                   ACTCCAACACT/	CCATGGGTGTAT	CCAGTGGGAGC/                 CCAGTGGGAGC/
Mismatches	SGTCTCGTTGGT 	GCACTGGGGCC 	CCTCCTCTGGAT 	TGGTGGAGCGAA               TGGTGGACCGAA	CTGTGTTAGACC 	AGCAGTCGGCTG 	SCATCATGGACC 	AGCTAGCTCAAA 	GGGAACGGGAGT               GGGAACGGGAGT	GGGTATCCGCT                  GGGTATCCGCT	agtctatgcaga                  agtctatgcaga	AGGGGACCCGAG 	CCTCCGAAGCAG 	TGGCGAAGGCCA                TGGCGAAGGCCA	ATAATGGAGATG                ATAATGGAGATG	AACTGGCCAAGG                 AACTGGCCAAGG	rggtggctcagg               rggtggctcagg	CAGACTCACTCT 
rvative 0;	AACCGCTCCGCT 	9990909990909 	SCTCCGGCCGCG 	AGGAGGCCTGGG 	ACATCCTCATCC 	rcaacgrgccrg 	CCTTTACCTGC 	ATGCCGTCACCC                 ATGCCGTCACCC	ACAAAGTCTTCC                ACAAAGTCTTCC	TECTGACTGCT 	CCGGGTGAAAG 	TTCTAGAGTCTG 	CCAGATCCTGG	CCAGTGCAGTTC 	TCTGACACAAC 	SCGCGTTCTCCA 	ATGTCACCAGCA                 ATGTCACCAGCA	rGCCAGGGACTO
88; Conse	GGCTTCTGGGAGCN	GAAATGCTGGCGCC	GGCTTCTGGCCGCC	TTCGTGCCGCAGCA	GAGCCTGGTTTGA/ 	AAGGAAATTGTCA1 	CAAATCGATGGAGI 	GAGGACCCTGAGTA 	AAACTCTCTNTGG/ 	GCCATCAACCAAGG	ATCCATGTGCCACC	AAACGGGCCACAGI	GGGAAGAAACAGGC 	GCAGCAGGAGAGGC 	CCTGGCTGCA 	GAGCAGTATGTCAC	TCCAACCCTGGCG/                TCCAACCCTGGCG/	CAAAGCCCCA 
Matches 11	1 60	61 GP 	121 GG 1121 GG	181 TT 	241 GP 241 GP 241 GP	301 AP	361 CP 361 CP	421 GP   1   421 GP	481 AP	541 GC 11 541 GC	601 AT    	661 AP 11 661 AP	721 GG 11 721 GG	781 GC 11 781 GC	841 AT       841 AT	901 GP 	961 TC    961 TC	1021 AC 11 1021 AC
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OY 1001 CAGGGTTACAACTAGGGACATAGGGACATAGGGACGGCGC 1140
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DD 1101 CAGGGTTACCAACTACAACTACAACTACAACTACAATTAGGCTTAGGCCT 1140
DD 1141 TGGGCTTACCACAGGCTCTGGGGACAACTACAACTACAATTAGCTTAT 1189
DD 1141 TGGGCTTACCAGGACTCTGGGGACAACTACAAATTACCATAT 1189
DD 1141 TGGGCTTACCAGGACTCTGGGGACAACTACAAATTACCATAT 1189
DD 1141 TGGGCTTACCAGGACTCTGGGGACAACTACAAATTACCAAATTATACTGATT 1189
DD 1141 TGGCCTTACCAGGACTCTGGGGACAACTACAAATTACCAAATTATACCAAATTATACCAAATTATACCAAATTATACCAAATTATACCAAATTACCAAATTATACCAAATTATACCAAATTATACCAAATTATACCAAATTATACCAAATTATACCAAATTATACCAAATTATACCAAATTATACCAAATTATACCAAATTATACCAAATTATACCAAATTACCAAATTATACCAAATTATACCAAATTATACCAAATTATACCAAATTATACCAAATTATACCAAATTATACCAAATTATACCAAATTATACCAAATTATACCAAATTATACCAAATTATACCAAATTACCAAATTATACCAAATTATACCAAATTATACCAAATTATACCAAATTATACCAAATTATACCAAATTACCA
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Length 16; 0; Indels

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Ouery Match 2.0%; Score 7; DB 1;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 7; Conservative 0; Mismatches
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APPLICANT: Lockshin, Curtis
APPLICANT: Lockshin, Laxander
APPLICANT: Lockshin, Alexander
APPLICANT: Holmes, Todd
APPLICANT: Holmes, Todd
APPLICANT: Holmes, Todd
APPLICANT: Holmes, Todd
TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
TITLE OF INVENTION: THEREPOR
TITLE OF INVENTION: HEREPOR
TITLE OF INVENTION: HEREPOR
TITLE OF INVENTION: HEREPOR
TITLE OF INVENTION: HOROR:
TONNERS HADDLE FORM:
ADDRESSE: HAMILTON BROOK, SMITH & REYNOLDS, P.C.
CITY: Lexington
CONPUTER: Two Militia Drive
STREE: HOPPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATION TYPE: Floppy disk
COMPUTER: Extentin Release #1.0, Version #1.25
APPLICATION UNBER: US/08/346,849
FILING DATE: SE DECEMBER 1992
APPLICATION NUMBER: US/09/3,326
FILING DATE: SE DECEMBER: MIT-6008
FILING DATE: SE DECEMBER: MIT-6008
FILING DATE: SE DECEMBER: MIT-6008
FILING DATE: BE DOOK, DAVIG E
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Patent No. 5670483
GENERAL INFORMATION:
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TYPE: amino acids
TOPOLOGY: linear
MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                       Kola, I. and Hertzog, P.J.
A novel member of the STOMATIN/EPB72/mec-2 family, stomatin-like 2 (STOML2), is ubiquitously expressed and localizes to HSA chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="SLP2"
//cote="member of the stomatin/band7/EPB72/MEC2 family;
//cote="member of the predicted Caenorhabditis elegans protein
similar to the predicted Caenorhabditis elegans MEC-2, and to the Homo
F30A10.5, to Caenorhabditis elegans MEC-2, and to the Homo
                                                            mRNA linear PRI 06-SEP-2001
2 (SLP2) mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (26-JUN-2000) Monash Institute of Reproduction and Development, Monash University, Monash Medical Centre, 246 Clayton Road, Clayton, Victoria 3168, Australia Location/Qualifiers
                                                                                                                                                                                                         Euteleostom1;
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czarek, C.M., Treutlein, H.R., Portbury, K.J., Gulluyan, L.M.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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/protein_id="AAF91466.1"
/db_xref="GI:9652259"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Owczarek,C.M., Treutlein,H.R.,
Kola,I. and Hertzog,P.J.
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/dev_stage="fetus"
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/gene="SLP2"
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Matches 957; Conservative
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1 (bases 1 to 1262)
Strausberg, R.
Direct Submission
Submitted (01-OCT-2001) National Institutes of Health, Mammalian
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/translation="MLARAARGTGALLLRGSLLASGRAPRRASSGLPRNTVVLFVPQO
BAWVERMSREHRILEBGLNILIPVLDRIRYVQSLKEIVINVPEGSAYTLDNYTLQID
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INQAADCWGIRCLRYEIKDIHVPPRVKESMOMOVEAERRRRATVLESEGTRESAINVA
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TVAEQYVSAFSKLAKDSNTILLPSNPGDVTSNVAQAMGVYGALTKAPVPGTPDSLSSG
SSRDVQGTDASLDEELDRVKMS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clone distribution: MGC clone distribution information can be four through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov series: IRAL Plate: 34 Row: p Column: 12.
This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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                                                                                                                                                                                                                        cDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) MA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada info@bcgsc.bc.ca
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/db_xref="LocusID:30968"
/db_xref="taxon:9606"
/clone="MGC:2325 IMAGE:4907745"
/tissue_type="Parceas, epithelioid carcinoma"
/clone_lib="NIH_MGC_42"
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/protein_id="AAH14990.1"
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                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Location/Qualifiers
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Matches 957; Conservative
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PUBLICATION INFORMATION:
DOCUMENT NUMBER: PCT/US92/08069
FILING DATE: 14-AUG-1993
US-08-152-488-3
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Length 29; Query Match 2.0%; Score 7; DB 1 Best Local Similarity 100.0%; Pred. No. 9.6 Matches 7; Conservative 0; Mismatches

Gaps ö

249 AKAKAKA 255

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US-08-152-488-3

Sequence 3, Application US/08152488 Patent No. 5534619

GENERAL INFORMATION:
APPLICANT: Wakefield, Thomas W.
APPLICANT: Andrews, Philip C.
APPLICANT: Stanley, James C.
TITLE OF INVENTION: NOVEL PEPTIDES, FOR HEPARIN AND TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN INUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Benita J, Rohm, Esq.
STREET: 512 Springfield avenue
CITRE: New Jersey

TELEFAX: 908-276-5533 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 29 amino acids

TYPE: amino acid STRANDEDNESS: N/

STATE: New Jersey
COUNTRY: United States of America
21P: 07016-181
. COMPUTER READABLE FORM:
MEDIDM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIDM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-D62
CURRENT APPLICATION DATA:
APPLICATION NOWBER: US/08/152,488
FILING DATE: 12-NOV-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NOWBER: PCT/US92/08069
FILING DATE: 14-NGC-1993
ATOMMER: ROAM: Benita J.
REGISTRATION NUMBER: 28,664
REFERENCE/DOCKET NUMBER: 28,664
REFERENCE/DOCKET NUMBER: RM-7MG
TELEMBHONE: 908-276-3344
MTTELEMBONE: 908-276-5344

TOPOLOGY: N/A MOLECULE TYPE: peptide ORIGINAL SOURCE:

ORGANISM: N/A UBLICATION INFORMATION:

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clone MGC:1179 IMAGE:3346384, mRNA,
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Catarrhini; Hominidae;
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Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
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Mammalia; Eutheria; Primates;
1 (bases 1 to 1278)
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Contact: MGC help des
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COMMENT
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Scries: IRAL Plates 5 Row: m Column: 8 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9652258.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EAWVVERMGRFHRILEPGLNILIPVLDRIRYVQSLKEIVINVPEQSAVTLDNVTLQID
GVILYLRINDPYKASYGVEDPEYAVTOLAQTYMRISELGKLSLDKVFRERESLINSIVDA
INQAADCWGIRCLRYEIKUHVPPRVKESWQMQVEAERRKRATVLESEGTRESAINVA
EGKKQAQILASEAERREQINQAAGERSAVLAKAKAKREAIRILAAALTOHNGDAASI.
TVAEQYVSAFSKLAKDSNTILLPSNPGDVTSNVAQAMGVYGALTKAPVPGTPDSLSSG
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                                                                                                                                 Contact: nisc_mogenhgri.nih.gov
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjanih,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Rarlins,E., Legaspi,R.,
Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MLARAARGTGALLLRGSLLASGRAPRRASSGLPRNTVVLFVPQQ
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
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/db_xxef="Locus10:3068"
/db_xref="Lacus10:30606"
/clone="MGC:1179 IMAGE:3346384"
/clone="MGC:1179 IMAGE:3346384"
/clone=lib="NIH_MGC_20"
/lab_host="DH108-R"
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Pred. No. 0;
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/protein_id="AAH02442.1"
/db_xref="GI:12803255"
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al Similarity 99.8%;
957; Conservative
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Wang, Y. and Morrow, J.S.
Identification and characterization of human SLP-2, a novel
homologue of stomatin (band 7.2b) present in erythrocytes and other
                                                                                                                                                                                                                                                                                                                                                                                                                                       mRNA linear PRI 13-MAR-2000 protein SLP-2 (HUSLP2) mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (25-SEP-1999) Pathology, Yale Medical School, 310-Cedar Street, New Haven, CT 06510, USA Location/Qualifiers
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          TCCTGGCCTCCGAAGCAGAAAAGCCTGAACAGATAAATCAGGCAGCAGCAGGAGGCCAGTG
                                                                                                                                                                                                                                                       TCTTCCGGGAACGGGAGTCCCTGAATGCCAGCATTGTGGATGCCATCAACCAAGCTGCTG
                                                                               TGAAAGAGTCTATGCAGATGCAGGTGGAGGCAGAGCGGCGGAAACGGGCCACAGTTCTAG
                                                                                                                     AGTCTGAGGGGACCCGAGAGTCGGCCATCAATGTGGCAGAAGGGAAGAAACAGGCCCAGA
                                                                                                                                                                                  TCCTGGCCTCCGAAGCAGAAAGGCTGAACAGATAAATCAGGCAGCAGAGGCCAGTG
                                                                                                                                                                                                    CAGTTCTGGCGAAGGCTAAAGCTGAAGCTATTCGAATCCTGGCTGCAGCTCTGA
                                                                                                                                                                                                                                           CACAACATAATGGAGATGCAGCATTCACTGACTGTGGCCGAGCAGTATGTCAGCGCGT
                                       ACTGCTGGGGTATCCGCTGCCTNCGTTATGAGATCAAGGATATCCATGTGCCACCCCGGG
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1. .1303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /chromosome="9
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Wang,Y. and Morrow,J.S.
Direct Submission
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AUTHORS
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REFERENCE
AUTHORS
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JOURNAL
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/product="membrane associated protein SLP-2"
/protein_id="AAF09142.1"
/db_xref="d1:6456118"
/translation="maraargranchirgsllasgraperrassgleprhtvulevp00
EAWVVERMGREHRILEPGLNILIPVLDRIRRYVQSLKEIVINVPEQSAVTLDNVTLQID
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INQADCWGIRCLRYEIKPENVESMQMQVEABRRKRATVLESEGTRESAINVA
EGKKQAQILASEBARRARDINQAAGEASAVLARAKARAREAIRILAAALTQHNGDAASL
TVAEQYVSAFSKLAKDSNYTLLLPSNPGDVTSWVAQAMGVYGALTKAFVPGTPDSLSSG
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                    /inote="stomatin-like protein 2; widely distributed peripheral membrane protein; similar to human erythrocyte stomatin and MEC 1 of Caenorhabditis elegans; thought to be involved in mechanoreception or lipid domain
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                                                                                                                                                                                                                                                                                                                                                                                                                      translation initiation site"
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99.8%; Pred. No. 0;
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/gene="HUSLP2"
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Isogai.T. and Otsuki.T.
Direct Submission
Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute,
Genomics Laboratory: 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomicsehri.co.jp, Tel:81-438-52-3951, Pas:81-438-52-3952)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; CDNA full insert sequencing:
Research Association for Blotechnology: cDNA library construction,
5'- & 3'-end one pass sequencing and clone selection: Helix
Research Institute (supported by Japan Key Technology Center etc.)
and Department of Virology, Institute of Medical Science,
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/clone_lib="NT2N1"
/note="cloning vector: pUC19FL3-mRNA from uninduced NT2
neuronal precursor cells."
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/db_xref="taxon:9606"
/clone="NT2RM1000080"
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Location/Qualifiers
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EGKKQAQILASEAEKAEQINQAAGEASAVLAKAKAKAEAIRILAAALTQHNGDAAASL
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Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Dietrich,N.L., Gunn,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspl,R.,
Lim,M., Maduro,O.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
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Eawwerngrehriepgimilipvldrirvvosikeiviuvpegsaytldnytlotd
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clone MGC:19715 IMAGE:3534656, mRNA,
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Submitted (02-UUL-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 27 Row: d Column: I that clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not
                                951 CCAGCATGGTGGCTCAGGCCATGGGTGTATATGGAGCCCTCACCAAAGCCCCCAGTGCCGG 1010
CCAGCATGGTGGCTCAGGCCATGGGTGTATATGGAGCCCTCACCAAAGCCCCAGTGCCAG 1039
                                                                     1040 GGACTCCAGACTCACTCTCCAGTGGGAGCAGCAGGATGTCCAGGGTACAGATGCAAGT 1098
                                                                                        1011 GGACTCCAGACTCACTCCAGTGGGAGCAGCAGAGATGTCCAGGGTACAGATGTCAAGT 1069
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Email: ggapbs r@mail.nih.gov
Tissue Procurement: DCTD/DTD
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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/db_xref="taxon:9606"
/clone="MGC:19715 IMAGE:3534656"
/clone=lib="NuH_MGC_7"
/lab_host="DH10B-R"
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nisc_mgc@nhgri.nih.gov
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/protein_id="AAH10152.1"
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SSRDVQGTDASLDEELDRVKMS"
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Jiang, Y., Harlocker, S.L. and Secrist, H.
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AX193464
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                  Sequence 193 from Patent WO0196388. AX339946
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Meagher, M. J., Xu, J. and King, G.E.
Compositions and methods for therapy and diagnosis of colon cancer
Patent: WO 0173027-A 1428 04-0CT-2001;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 518)
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                                                      Au,J., Lodes,M.J., Secrist,H., Benson,D.R., Meagher,M.J., Stolk,J.A., King,G.E., Wang,T. and Jiang,Y. Compounds for immunotherapy and diagnosis of colon cancer methods for their use
Patent: WC 0149716-A 1031 12-JUL-2001;
CORIXA CORPORATION (US)
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AX261777
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                                                                                                                                                                                                                                                                       109
                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
136 c 149 g 1(
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                 200 CCTGGGTGGTGGAGCGAATGGGCCGATTCCACCGGATCCTGGAGCCTGGTTTGAACATCC 259
                                                                                                              Gaps
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Jiang,Y., Dillon,D.C., Mitcham,J.L., Xu,J., Harlocker,S.L.
Hepler,W.T.
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Sequence 26 from Patent WO0179286.
AX302706
AX302706.1 GI:17383208
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/db_xref="taxon:9606"
96 c 72 g 85
                     1. 691
/organism="Homo sapiens"
/db_xref="taxon:9606"
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1. .301
  CORIXA CORPORATION (US)
Location/Qualifiers
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Best Local S:
Matches 381
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AC026501 55406 bp DNA 11near HTG 22-MAR-2000
Homo sapiens chromosome 1 clone RP11-266M12 map 1, LOW-PASS
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        PAT 26-0CT-2001
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Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                   Meagher, M.J., Xu, J. and King, G.E. Compositions and methods for therapy and diagnosis of colon Patent: WO 0173027-A 596 04-OCT-2001;
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          linear
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Pred. No. 5.8e-90;
0; Mismatches 1;
          DNA
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Sequence 596 from Patent WO0173027.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
| 181 c 169 g 159
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99.5%;
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Matches 219; Conservative
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AC026501/c
LOCUS
DEFINITION
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bp in length

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10363: gap of 100 bp 11053: cont.ig of 690 bp in length 11033: gap of 100 bp 11133: gap of 100 bp 11134: gap of 100 bp 11239; cont.ig of 691 bp in length 1012799: gap of 100 bp 1012799: gap of 100 bp 1012799: gap of 100 bp 1013444: cont.ig of 705 bp in length 1012799: gap of 100 bp 1013444: cont.ig of 705 bp in length
                                                                                                                                     100 bp
if 709 bp in length
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f 683 bp in length
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    gap of
    100 bp

    7: contig of 693 bp i

    gap of
    100 bp

    7: contig of 710 bp

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contig of 709 bp i
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contig of 703 bp i
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f 714 bp
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33270: contig of 711 bp
33370: gap of 100 bp
34172: gap of 100 bp
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28457: contig of 678 bp
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13545 14237: cont.
14238 14337: gap of
14338 15047: cont.
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31656: 756.
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                                                                                                                                                                                                                                                                                                                                                                                                                          Sire J. (Dassa I to 25406)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boukhalater, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Castle, A., Castle, R., Brown, A., Burkett, G., Campopiano, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Karatas, Howland, J.C., Illev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lancque, K., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lakoque, K., Landares, R., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, R., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Minova, T., Minova, T., O'Donnor, T., O'Donnoll, P., Pisani, C., Pollara, V., Raymond, C., Riley, S., Sepecer, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Spencer, S., Severy, P., Spencer, N., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Voung, G., Zahnoun, J., Zimmer, A. and Zody, M., Trigillo, J., Voung, G., Zimmer, A. and Zody, M., Wyman, D., Ye, W. J., Voung, G., Zhmer, A., And Zody, M., Trigillo, J., Maner, A., Jahan, J., J
                                                                                                                                                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (22-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------ Genome Center,
Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 bp
f 718 bp in length
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if 685 bp in length
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                                                                                                                                                                                                                                                                                                Birchen, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 1, clone RP11-266M12 Unpublished
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Center clone name: 266_M_12
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3052: con
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3870: con
                                    AC026501
AC026501.1 GI:7283191
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5475:
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SEQUENCE SAMPLING.
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                     ACCESSION
VERSION
KEYWORDS
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AUTHORS
TITLE
JOURNAL
REFERENCE
                                                                                                                                                                     ORGANISM
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JOURNAL
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Lamerdin, J.E., McCready, P.M., Skowronski, E., Adamson, A.W.,
Burkhart-Schultz, K., Gordon, L., Kyle, A., Ramirez, M., Stilwagen, S.,
Phan, H., Velasco, N., Garnes, J., Danganan, L., Poundstone, P.,
Christensen, M., Georgescu, A., Avila, J., Liu, S., Attix, C.,
Andreise, T., Tranhelm, M., Amico-Keller, G., Coefield, J., Duarte, S.,
Locas, S., Bruce, R., Thomas, P., Quan, G., Krommiller, B., Arellano, A.,
Montgomery, M., Ow, D., Nolan, M., Trong, S., Kobayashi, A., Olsen, A.O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (25-MAR-1998) Joint Genome Institute, Lawrence Livermore
National Laboratory, 7000 East Ave., Livermore, CA 94551, USA
Location/Qualifiers
                                                                                                                                                                        Euteleostom1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence analysis of a human Pl clone containing the XRCC9 DNA repair gene Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="Fibroblast or foreskin"
/lab.host="NS316"
/note="Pl clone obtained from Genome Systems, Inc."
complement(4. .80)
  sapiens chromosome 9, Pl clone 11659, complete sequence
                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/rpt_family="aluy"
complement(402. 626)
complement(707. 1338)
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rpt_family="MER4_internal"
534. 5723
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/rpt_family="MER4_internal"
complement(7560. 8234)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
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omplement(1)10
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/rpt_family="HERVH"
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/rpt_family="MER83"
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/rpt_family="HERVH"
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/rpt_family="LTR7"
complement(5036. 5621)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(6027. 6110)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(1742. .3015)
/rpt_family="HERVH"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /rpt_family="HERVH" complement(1361. .1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /map="9p13"
/clone="P1.11659"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /chromosome="9"
                                                         AC004472.1 GI:2984582
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Lamerdin, J.E.
                                                                                                                                                                                                                           (bases 1 to 86765)
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                                                                       35631 35730: gap of 100 bp 35731 363135730: gap of 100 bp 36343 53520: contig of 705 bp in length 36343 53220: contig of 685 bp in length 37221 37220: gap of 100 bp 37321 37320: gap of 100 bp 37321 37320: gap of 100 bp 37321 37320: gap of 100 bp 38632: gap of 100 bp 38633 38777: contig of 655 bp in length 38633 38777: contig of 655 bp in length
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                                                35630: contig of 694 bp in length
30: gap of 100 bp
36435: contig of 705 bp in length
                                                                                                                                                                                                                                                                                                                                                         39660: gap of 100 bp
40347: contig of 687 bp in length
4047: gap of 100 bp
41129: contig of 682 bp in length
41229: gap of 100 bp
41927: contig of 698 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42027: gap of 100 bp
42733: contig of 706 bp in length
4283: gap of 100 bp
4316: contig of 633 bp in length
43616: gap of 100 bp
44335: contig of 719 bp in length
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54717: gap of 100 bp
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683 bp in length
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100.0%; Pred. No. ...
0; Mismatches
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53822: contig of 7
                      34936: gap of 1
35630: contig of
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51431: con+
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54617: cont
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Matches 149; Conservative
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8239. .9165 /rpt\_family="MSTB-internal" complement(9215. .9483)

rpt\_family="MER4A"

repeat\_region

PRI 15-JUN-2001

linear

DNA

86765 bp

AC004472

RESULT 15 AC004472/c LOCUS

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complement(29214. 29339)
/note="predicted exon, program:
frame: 0, quality: good, score:
complement(29628. 29915)
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Live 0; Mismatches 0;
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complement'??
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27727. 2802.
                                                                                                                                                                                             complement(21324. 21361)
/rpt_family="MIR"
21365. 21487
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complement(27334. .27637)
                                                                                                                      /rpt_family="LINE2"
complement(20739. .21323)
/rpt_family="LTR10C"
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complement(26831. .27035)
/rpt_family="MLT1D"
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                                                                           /rpt_family="LINE2"
20258. .20313
                           'rpt_family="Aluy"
.9288. .20021
                                                                                                                                                                                                                                                  .21487
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/rpt_family="AluJo"

n 17540 .17397

/rpt_family="AluJo"

/rpt_family="AluJo"

/rpt_family="AluJo"

/rpt_family="AluJo"

/rpt_family="AluJo"

17714 .18004

/rote="DDS similarity to overlapping ESTs:

(17728 .18004) AA054173 zf51a08r1 Soares retina N2b4HR

Homo sapiens cDNA clone 380438 5' similar to contains Alu

repetitive element; (276 .1); 99% identity.

(18004 .17714) A013121 ze56c07 r1s Soares retina N2b4HR

Homo sapiens cDNA clone 360108 5' similar to contains Alu

repetitive element; (1 .292); 97% identity.-(18004 .17714)

AA01750z ze38h03.r1 Soares retina N2b4HR Homo sapiens cDNA

clone 361301 5' similar to contains Alu repetitive

element; Score: 567 Identity: 292/297 (98%).".*.

/rpt_family="AluJo"

/rpt_family="AluJo"
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//rpt_family="Alusg"
//rpt_family="Alusg"
| 15118. .15404
//rpt_family="Alusg"
| 15134. .15604
//rpt_family="Alusg"
| 15134. .15604
//rpt="DDS similarity to overlapping ESTS:
//roct="DDS similarity to overlapping ESTS:
//r
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                      1484. .9748
rpt_family="MSTB-internal"
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/rpt_family="POLY_A"
complement(17033. .17060)
/rpt_family="AT_rich"
17101. .17239
                                                                                                                                                            rpt_family="Alusg"
1777. .12076
                                                                                             /rpt_family="MSTB"
complement(10291. 10484)
/rpt_family="AluJo"
complement(10495. 10794)
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rpt_family="(TAAA)n"
2479. .12775
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16932. .16978
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4620. .14895
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2077. 1910s
/rpt_family="AluJo"
9484. .9748
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3945. .14247
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4504. .14618
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rpt_family="AluSq"
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Human; integral membrane protein; IMP; cancer; anaemia; prostate;
breast; pancreatic; tumour; ion transport; ss.
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/transl_except= (pos:490..492,aa:Xaa)
/transl_except= (pos:1099..1101,aa:Xaa)
/note= "Xaa= unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human integral membrane protein encoding DNA
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AAZ13550
AAX98374
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AAK50720
AAI27734
AAI56701
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AAS58068
AAC17814
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AAT19309
         AAS58752
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1 GGCTTCTGGGAGCNACCGCT......GGAAGCAGATTTTCCTGATT 1188
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AAX04345
ABA09225
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AAX13961
AAH13961
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Copyright (c) 1993
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The present sequence encodes human integral membrane protein (IMP). IMP may be administered to a subject to treat disorders associated with abnormal ion transport or membrane conductance as well as a variety of tumours, e.g. haemolytic anaemias and prostate, breast and pancreatic tumours. A vector capable of expressing IMP, or a fragment or a derivative thereof, may also be administered to a subject to treat the haemolytic anaemias and prostate, breast and pancreatic tumours.
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                                                                                recombinant protein, for treatment of anaemia and cancer
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llarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
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Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; ATDS; ospitity edisorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroidtis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                                                                                                                                               TCCAACCCTGGCGATGTCACCAGCATGGTGGCTCAGGCCATGGGTGTATATGGAGCCCTC 1020
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Y, Young P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated human genes and the secreted polypeptides they encoduseful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
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                                                                                                                                                                                                  P, Greene JM,
Ruben SM, Shi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1337 BP; 338 A; 346 C; 377 G; 273 T; 3 other;
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sen HS, Rosen CA,
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       9705-0052989.
9705-0051919.
9705-0055984.
9705-0058665.
9705-0058669.
                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC
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Olsen HS,
                                                                                                               97US-0060834.
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Matches 957; Conservative
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                  08-JUL-1997;
18-AUG-1997;
12-SEP-1997;
12-SEP-1997;
12-SEP-1997;
                                                                               12-SEP-1997;
12-SEP-1997;
12-SEP-1997;
                                                                                                                02-OCT-1997
                                                                       12-SEP-1997
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Human; cytokine; cell proliferation; cell differentiation; growth factor haematopoiesis regulation; tissue growth; immunomodulator; activin; inhibin; chemctaxis; chemckinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; lymphold cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antinilammatory; antiarthritic; haemostatic; antiarteriosclerotic; cytostatic; osteopathic; vasculopic; cardiant; virucide; antibacterial; antifungal; vulnerary; antiulcer; ss.
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                                                     TCTTCCGGGAACGGGAGTCCCTGAATGCCAGCATTGTGGATGCCATCAACCAAGCTGCTG
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                                                                                                                                                                                                                                                                                  TGAAAGAGTCTATGCAGATGCAGGTGGAGGCAGAGCGGCGGAAACGGGCCACAGTTCTAG
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                                                                                                                                                                                                                                                                                                                   Human SLP-2 homologue-encoding cDNA, SEQ ID NO:1001.
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Drmanac RT
          05-FEB-2001; 2001WO-US03800
               2000US-0496914
                  2000US-0560875
                                 2001-457740/49.
                            Tang YT, Liu C,
                       (HYSE-) HYSEQ INC
                                    P-PSDB; ABB11981
WO200157188-A2
               03-FEB-2000;
27-APR-2000;
     09-AUG-2001
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Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis and cancer

Claim 1; Page 851; 1963pp; English.

Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and invention also relates to vectors and recombinant host cells comprising a nucleation also relates to vectors and recombinant host cells comprising a nucleation also relates to vectors and recombinant host cells comprising a nucleation also relates to vectors and recombinant host cells comprising an uncleation of the invention. Methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence comprehensive the invention have belongical activities, and hence of premoteration activities; stem cell growth factor activity; and effected activity; immunomodulatory activity; sincel growth activity; and effected activity; immunomodulatory activity; issue growth activity; immunomodulatory activity; activities; haemostatic conference of the moderation activity; in moderatic or chemokinetic activities; haemostatic, thrombotic or thrombotic activity; and activities; or may be involved in oncogenesis, cancer cell proliferation or metastasis.

Cohemotactic or chemokinetic activities; haemostatic, thrombotic or thrombotic activity; and protein or gene therapy. Such conditions include conditions on their biological activities; bracking conditions include conditions, e.g., by protein or gene therapy. Such conditions include conditions, e.g., by protein or gene therapy. Such conditions include conditions, e.g., by protein or gene therapy. Such conditions include conditions, e.g., by protein or gene therapy. Such conditions include conditions include acides encoding them) may be used to promote wound the alsomethy. Polypeptides modely with tissue regeneration and conditions in declinate activity may be used in the treatment of viral, bacterial and fungal infections in addition to immune disease or accidental damage. The polypeptides with growth factor activity may be used in the d ling techniques. The present sequence represents a cDNA encoding a human polypeptide of the invention.

Sequence 1398 BP; 307 A; 408 C; 359 G; 324 T; 0 other;

ö GCCGCGCCTCCTCTGGATTGCCCCGAAACACCGTGGTACTGTTCGTGCCGCAGCAGGAGG 1195 GCCGCGCCTCCTCTGGATTGCCCCGAAACACCGTGGTACTGTTCGTGCCGCAGCAGGAGG 199 Gaps ; 0 Length 1398; Indels 2 DB 22; Score 857; DB Pred. No. 0; 0; Mismatches 0; 72.1%; 99.8%; Conservative al Similarity 957; Conserv Query Match Best Local S Matches 140 1254 g

CCTGGGTGGTGGAGCGAATGGGCCGATTCCACCGGATCCTGGAGCCTGGTTTGAACATCC 259

200

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1015 CCAGCATGGTGGCTCAGGCCATGGGTGTATATGGAGCCCTCACCAAAGCCCCAGTGCCAG 1039 1194 CTGGGTGGTGGTGGAATGGGCCGATTCCACCGGATCCTGGAGCCTGGTTTGAACATCC 1135 439 895 619 775 199 859 AGTCTGAGGGGACCCGAGAGTCGGCCATCAATGTGGCAGAAGGGGAAGAACAGGCCCAGA 739 TCTCCAAACTGGCCAAGGACTCCAACACTATCCTACTGCCCTCCAACCCTGGCGATGTCA 979 TCATCCCTGTGTTAGACCGGATCCGATATGTGCAGAGTCTCAAGGAAATTGTCATCAACG 1014 ACCTGCGCATCATGGACCCTTACAAGGCAAGCTACGGTGTGGAGGACCCTGAGTATGCCG ACTGCTGGGGTATCCGCTGCCTNCGTTATGAGATCAAGGATATCCATGTGCCACCCCGGG TGAAAGAGTCTATGCAGATGCAGGTGGAGGCAGAGCGGCGGAAACGGGCCACAGTTCTAG CAGTTCTGGCGAAGGCCAAGGCTAAAGCTGAAGCTATTCGAATCCTGGCTGCAGCTCTGA CACAACATAATGGAGATGCAGCTTCACTGACTGTGGCCGAGCAGTATGTCAGCGCGT TGCCTGAGCAGTCGGCTGTGAGTCTCGACAATGTAACTCTGCAAATCGATGGAGTCCTTT ACCTGCGCATCATGGACCCTTACAAGGCAAGCTACGGTGTGGAGGACCCTGAGTATGCCG TCACCCAGCTAGCTCAAACAACCATGAGATCAGAGCTCGGCAAACTCTCTNTGGACAAAG TCTTCCGGGAACGGGAGTCCCTGAATGCCAGCATTGTGGGATGCCATCAACCAAGCTGCTG TCCTGGCCTCCGAAGCAGAAAAGGCTGAACAGATAAATCAGGCAGCAGGAGAGGCCAGTG Human polynucleotide SEQ ID NO 2212. BP. RESULT 4 AAK52683/c ID AAK52683 standard; CDNA; 1398 (first entry) 06-NOV-2001 AAK52683; 260 380 1134 320 1074 560 089 1040 440 954 200 894 834 620 774 714 740 654 800 594 860 534 920 474 980 414 g g . G q QQ qq δy δλ ò ò δy q ò δy g δy qq 셤 ò qq ò q ò g δ q δ

Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.

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CCAGCATGGTGGCTCAGGCCATGGGTGTATATGGAGCCCTCACCAAAGCCCCAGTGCCAG 1039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;
                                                                                                                                                    TCCTGGCCTCCGAAGCAGAAAAGGCTGAACAGATAAATCAGGCAGCAGGAGAGAGGCCAGTG
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                                 TCTTCCGGGAACGGGAGTCCCTGAATGCCAGCATTGTGGATGCCATCAACCAAGCTGCTG
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                                                                                                                                  ACTGCTGGGGTATCCGCTGCCTNCGTTATGAGATCAAGGATATCCATGTGCCACCCCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           encoding novel human secretory protein, Seq ID No 34.
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                                                                                                                                                                                                                                                                                                                      Ma Y;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding polypeptides with cytokine-like activities useful in diagnosis and gene therapy \dot{\gamma}
                                                                                                                                                                                                                                                                                                                    Cao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .,
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ang J, Ren F, Chen
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                                                                                                                                                                                                                                                                                                                                  Wang J, Zhang J, Ren | Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 4572; 6221pp; English.
                                                                                                                                                                                                               2000US-0663561.
2000US-0693325.
2000US-0728422.
                                                                                                                                                                                                                                                                                                                      Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72.1%;
99.8%;
                                                                                                 2001WO-US04098
                                                                                                                                                    20000S-0560875
                                                                                                                                                                2000US-0598075.
2000US-0620325.
                                                                                                                                                                                                   2000US-0654936
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Best Local Similarity 99.8
Matches 957; Conservative
                                                                                                                                                                                                                                                                                                                                                                                   2001-476283/51
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Wang D,
Yang Y, W
                                                                                                                                                                                                                                                                                     (HYSE-) HYSEQ INC
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P-PSDB; AAM79550
                                 WO200157190-A2
                                                                                                                                                                                                 01-SEP-2000;
15-SEP-2000;
20-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inflammation
 Homo sapiens
                                                                                               05-FEB-2001;
                                                                                                                                                                20-JUN-2000;
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                                                                                                                                                                                                                                                                                                                  Tang YT,
Zhao QA,
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The invention relates to novel isolated human secreted polypeptides (I) and polypucleotides (II). (I) and (II) are useful for treating influence and polypucleotides (II). (I) and (II) are useful for treating inclusion injury, shock, sepsis, immune responses, and is involved in increasing haematopoiesis, stem cell survival, bone growth and remodeling; (I), (II) and modulators of (II) are useful for prophylaxis or treatment of one or more cancers. (II) is also useful for prophylaxis or treatment of one or studying the in vivo activities of the polypeptide as well as for studying the in vivo activities of the polypeptides. (I) induces the proliferation of neural cells and regeneration of nerve and brain tissue and is useful for the treatment of central and peripheral nervous system diseases and neuropathies, such as Alzheimer's, Parkinson's disease, Huntington's disease, and amyotrophic lateral call asorders, in addition, (I) is involved in chemotactic or chemokinetic activity, regulation of haematopoiesis and is useful for treating myaeloid or lymphoid cell disorders, platelet disorders such as thrombocytopenia culcers, for treating ostboorosis, osteoarthritis, bone degenerative culcers, for treating osteoporosis, osteoarthritis, bone degenerative culcers, for treating osteoporosis, osteoarthritis, bone degenerative culcertion or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, various immune deficiencies and fibroders including severe combined immunodeficiency (SCID), beterial or fibroders including severe combined immunodeficiency (SCID), beterial or fibroders including severe combined immunodeficiency (SCID), beterial or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fungal infections, autoimmune disorders e.g. multiple sclerosis, rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic reactions and conditions, such as asthma or other respiratory problems. In addition, (I) affects biorhythms or circadian cycles of rhythms, fertility, metabolism, catabolism, anabolism, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides analgesic effects or other pain reducing effects, immunoglobulin like activity and can act as an antigen in a vaccine composition to raise an immune response. Ask44920-Ask55295 represent novel human secreted protein
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Wang
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AJ,
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Yang Y,
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20-OCT-2000;
               07-MAR-2000;
19-MAY-2000;
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14-JUL-2000;
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Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue, cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obsetty; osteoclast; thyuus; osteoporosis; arthitis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
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   TGCCTGAGCAGTCGGCTGTGACTCTCGACAATGTAACTCTGCAAATCGATGGAGTCCTTT
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Y, Young P;
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en HS, Rosen CA, Ruben SM, Shi
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Ni J, Olsen HS,
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           sapiens
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Query Match

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                                                       CAACATAATGGAGATGCAGCAGCTTCACTGACTGTGGCCGAGCAGTATGTCAGCGCGTTC
                                    CGCGCCTCCTCTGGATTGCCCCGAAACACCGTGGTACTGTTCGTGCCGCAGCAGGAGGCC
                                                                                                           TGGGTGGTGGAGCGAATGGGCCGATTCCACCGGATCCTGGAGCCTGGTTTGAACATCCTC
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Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length CDNAs.
                                       Human; primer; detection; diagnosis; antisense therapy; gene
                                                                                                                                                                                            Saito K, Y
Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1244 BP; 284 A; 327 C; 368 G; 265 T; 0 other;
                                                                                                                                                                                                                                                                            8; SEQ ID 11009; 2537pp + CD ROM; English
                                                                                                                                                                                           Hayashi K, S
A, Nagai K,
                      Human cDNA sequence SEQ ID NO:11009
                                                                                                                                                                                                    Wakamatsu
                                                                                                                                 99JP-0300253.
2000JP-0118776.
2000JP-0183767.
                                                                                                                                                                                            Isogai T, Nishikawa
Sugiyama T, Wakama
                                                                                                          2000EP-0116126
                                                                                                                          99JP-0248036
                                                                                                                                                           2000JP-0241899
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                                                                                                                                                                             (HELI-) HELIX RES INST
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                                                                                                                                  27-AUG-1999;
11-JAN-2000;
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                                                                                                                                                            09-JUN-2000;
                                                                          EP1074617-A2
                                                          Homo sapiens
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       26-JUN-2001
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Ishii S
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(first entry)
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The present invention describes primer sets for synthesising 5602

(111-length cDNAs defined in the specification. Where a primer set
comprises: (a) an oligo-dT primer and an oligonucleotide complementary
comprises: (a) an oligo-dT primer and an oligonucleotide complementary
to the complementary strand of a polynucleotide which comprises one of
the 5602 nucleotide comprises at least 15 nucleotides; or (b) a combination
of an oligonucleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence complementary to a
polynucleotide which comprises at least 15 nucleotides and the combination of
the 5'-end sequence 3'-end sequence 15 selected from those defined in
the specification. The primer sets can be used in antisense therapy and
in gene therapy. The primers are useful for synthesising polynucleotides,
particularly full-length cDNAs. The primers are also useful for the
certection and/or diagnosis of the abnormality of the proteins encoded by
the full-length cDNAs. The primers are also useful for the
cDNAs easily without any specialised methods. AAH03618 and
AAH03633 represent human amino acid sequences; AAB92446 to
AAH036393 represent human amino acid sequences; and AAH13629 to AAH13632
crepresent oligonucleotides, all of which are used in the exemplification
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ilarity 99.7%;
Conservative
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Best Local Similarity
Matches 956; Conserv
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Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
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                             tcatccctgtgttagaccggatccgatatgtgcagagtctcaaggaaattgtcatcaacg
                                                     TGCCTGAGCAGTCGGCTGTGACTCTCGACAATGTAACTCTGCAAATCGATGGAGTCCTTT
                                                                                                          ACCTGCGCATCATGGACCCTTACAAGGCAAGCTACGGTGTGGAGGACCCTGAGTATGCCG
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                                                             TCTTCCGGGAACGGGAGTCCCTGAATGCCAGCATTGTGGATGCCATCAACCAAGCTGCTG
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immunogenic; gene therapy; vaccine; colonic cancer;
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20000S-0504629.
20000S-0519444.
20000S-0675251.
20000S-0609448.
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E, Wang T,
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15-FEB-2000;
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19-MAY-2000;
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King GE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or
                                                                                                                                                                                                                                                                                                                                                        Υ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tcatccctgtgtttagaccggatccgatatgtgcagagtctcaaggaaattgtcatcaacg 329
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                                                                                                                                                                                                                                                                                                                                                          Ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding polypeptides with cytokine-like activities,
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. Wang ZW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                                                                                                                                                                                                                      V, Zhou P,
Ren F, Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5;
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lang J, Ren F
Goodrich R;
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llarity 99.8%; Pred. No. 0;
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 1135-1136; 6221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 useful in diagnosis and gene therapy
                                                                                                                                                                                                                                                                                                                                                                      zhang
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Zhao QA, Wang D, Wang J, Zh:
Xue AJ, Yang Y, Wejhrman T,
                                                                                                                                                                                                             2000US-0654936.
2000US-0663561.
2000US-0693325.
2000US-0728422.
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2000US-0560875.
2000US-0598075.
2000US-0620325.
                                                                                             2001WO-US04098
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Matches 893; Conserv
                                                                                                                                                                                                                                                                                                               (HYSE-) HYSEQ INC.
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                WO200157190-A2.
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                                                                                             05-FEB-2001;
                                                         09-AUG-2001
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                                                                                                     The present invention describes colon tumour associated proteins (I) and (II) can be used in gene therapy and vaccine production. (I) and (II) can be used in gene therapy and vaccine production. (I) and (II) can be used in the prevention, diagnosis and treatment of diseases associated with inappropriate colon tumour associated protein (TCAP) expression, such as colonic cancer. For example, (I) and (II) may be used to treat disorders associated with decreased expression by credity in mutations or deletions in a patient's genome that affect the activity of TCAPs by expressing inactive proteins or to supplement the production of them. Additionally, (II) may be used to complementary sequences may also be used as DNA probes in diagnostic complementary sequences may also be used as DNA probes in diagnostic complementary sequences may also be used as DNA probes in diagnostic cupin reaction (FCR) and hybridisation assays to detect and quantitate the presence of similar nucleic acids in samples, and theoretore which patients may be in need of restorative therapy. (I) may and in assays to identify modulators of TCAP expression and activity.

Anti-(I) antibodies and antagonists may also be used to down regulate the presence of similar nucleic acids in samples.

Anti-(I) antibodies and antagonists may also be used to down regulate the prepression and activity. The anti-(I) antibodies may also be used as diagnostic agents for detecting the presence of TCAPs expression and activity.

Anti-(I) antibodies and antagonists may also be used to down regulate (e.g. by enzyme linked immunosorbant assay (ELISA). AAI2460 to AAI29512 envent in the examples.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Colon tumor associated proteins and nucleic acids useful for prevention, diagnosis and treatment of colonic cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 518 BP; 123 A; 136 C; 149 G; 109 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 365; DB 22;
Pred. No. 4.5e-169;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          680 AGTCTGAGGGGACCCGAGAGTCGGCCATCAATGTGGCA 717
                                                                Claim 2; Page 415; 472pp; English
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99.4%;
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Matches 515; Conserv
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The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been sisolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence was used as the representative sequence from a human clone which was used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    homology searches to identify the clone.
Note: The sequence data for this patent did not form part of the printed
specification, but was obtained in CD-ROM format directly from EPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Primers useful for synthesizing full length cDNA clones and their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTGAACAGATAAATCAGGCAGCAGGAGAGGCCAGTGCAGTTCTGGCGAAGGCCAAGGCTA 823
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       al T, Hayashi K, Ishii S, Kawai Y;
Nagai K, Kojima S, Otsuki T, Koga
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                                                                                                                                                                                                                                                                                                                                                                                  Human; full length cDNA; cDNA synthesis; oligo-capping; ss
                                                                                                                                                                                                                                                                                                                            Human cDNA clone representative sequence, SEQ ID NO: 2385.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28.2%; Score 335; DB 22; L larity 100.0%; Pred. No. 2.4e-154; Conservative 0; Mismatches 0;
use in genetic manipulation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       kawa T, Isogai
Sugiyama T, Na
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11-JAN-2000; 2000JP-0118774.
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                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                           AAK93925 standard; cDNA;
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nes 335; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wakamatsu A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EP1130094-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                      06-NOV-2001
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                                                                                                                                                                                                                   AAK93925;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Th present invention relates to the isolation of novel cDNA sequences encoding for at least an immunogenic portion of human colon tumour proteins. The sequences of the invention are useful in pharmaceutical compositions and vaccines for the prevention and treatment of cancers such as colon cancer. They are also useful for the diagnosis and monitoring of such cancers. Antibodies to the colon tumour proteins and antigen presenting cells that express polynucleotides encoding colon tumour proteins can be used to inhibit the development of cancers. T-cells that react specifically with colon tumour proteins are useful for removing tumour cells from samples (e.g. blood) and for cancer treatment. The polynucleotides sequences are also useful in gene therapy. AAS$7325-AAS$880 represent the cDNA sequences of the invention that encode for portions of human colon tumour proteins.
ACACTATCCTACTGCCCTCCAACCCTGGCGATGTCACCAGCATGGTGGTGGTCAGGCCATGG 1003
                                                         Human; colon tumour protein; colon cancer; gene therapy; cytostatic;
                                                                          New colon tumour proteins and related nucleic acid, useful for treatment, prevention, diagnosis and monitoring of cancer -
                                                                                                                                                                                                                                                                                                           cDNA #1428 encoding portion of a human colon tumour protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 691 BP; 183 A; 168 C; 184 G; 140 T; 16 other;
                                                                                                                  GGAGCAGCAGAGATGTCCAGGGTACAGATGCAAGT 1098
                                                                                                                                 GGAGCAGCAGATGTCCAGGGTACAGATGCAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; Page 281; 299pp; English.
                                                                                                                                                                                                                        BP.
                                                                                                                                                                                                                      AAS58752 standard; cDNA; 691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-MAR-2000; 2000US-191597P.
04-MAY-2000; 2000US-202024P.
05-MAY-2000; 2000US-202189P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               King GE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-MAR-2001; 2001WO-US09246
                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CORI-) CORIXA CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Meagher MJ, Xu J,
                                                                                                                                                                                                                                                                                                                                                                                                    WO200173027-A2
                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a full length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human cDNA of the invention.
Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        830 Primers useful for synthesizing full length cDNA clones and their use in genetic manipulation \dot{\cdot}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
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Ishii S, Kawai Y;
S, Otsuki T, Koga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 8; SEQ ID NO 3958; 1380pp + sequence listing; English.
                                                                                                                                                                                                                                                                                      Human; full length cDNA; cDNA synthesis; oligo-capping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isogai T, Hayashi K, Is
T, Nagai K, Kojima S,
                                                                                                                                                                                                                                                       Human full-length cDNA, SEQ ID NO: 3958
                                                                                                                                                            ВР
                                                                560 ACTGCTGGGGTATCCGCTGCCT 581
                                                                                                                                                          AAK94818 standard; cDNA; 2064
                                                                                                                                                                                                                                                                                                                                                                                                                                             08-JUL-1999; 99JP-0194486.
11-JAN-2000; 2000JP-0118774.
02-MAY-2000; 2000JP-0183765.
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                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-524255/58.
P-PSDB; AAM93862.
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                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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Gaps

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Indels

Length 691;

Score 331; DB 23; Pred. No. 2.2e-152;

27.9%; 99.7%;

0; Mismatches

Conservative

Query Match Best Local Similarity Matches 381; Conserv

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CCTGGGTGGTGGAGCGAATGGGCCGATTCCACCGGATCCTGGAGCCTGGTTTGAACATCC 259

cetgggtggtggagcgaatgggccgattccaccggatcctggagcctggtttgaacatcc 60

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25-OCT-2001
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                                                                                                                                                                                                 gctgaacagataaatcaggcagcaggagaggccagtgcagttctggcgaaggccaaggct 1408
                                                                                                                        762
                                                                             642
                                                                                                                702
                                                             Gaps
specification, but was obtained in CD-ROM format directly from EPO
                                                                             CGTTATGAGATCAAGGATATCCATGTGCCACCCCGGGTGAAAGAGTCTATGCAGATGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New peptide useful as a marker for the diagnosis of breast cancer
                                                                                                                GTGGAGGCAGAGCGGCGGAAACGGGCCACAGTTCTAGAGTCTGAGGGGACCCGAGAGTCG
                                                                                                                                                 GCCATCAATGTGGCAGAAGGGAAGAACAGGCCCAGATCCTGGCCTCCGAAGCAGAAAAG
                                                                                                                                                                                   763 GCTGAACAGATAAATCAGGCAGCAGGAGGCCAGTGCAGTTCTGGCGAAGGCCAAGGCT
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                                          Length 2064;
                                                            0; Indels
                                                                                                                                                                                                                             823 AAAGCTGAAGCTATTCGAATCCTGGCTGCAGCTCTGACACAACAT 867
                 581 G; 498 T; 0 other;
                                                                                                                                                                                                                                                                                                                                    cancer expressed polynucleotide 15952
                                                                                                                                                                                                                                                                                                                                                    Human; breast cancer; cell marker; cytostatic; ss
                                           Score 285; DB 22;
Pred. No. 8.4e-130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
                                                            0; Mismatches
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                   Sequence 2064 BP; 479 A; 506 C;
                                           24.0%; ; 100.0%;
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2000US-0192099.
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2000US-0205230.
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                                           Query Match 24.0
Best Local Similarity 100.
Matches 285; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wang
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                                                                                                                                                                                                                                                                                                                                                                                     WO200151628-A2
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14-MAR-2000;
24-MAR-2000;
                                                                                                                                                                                                                                                                                                                                    Human breast
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15-MAY-2000;
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25-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                        detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polynucleotides and encoded polypeptides are also useful for isolating compounds with cytostatic
                                                                                                                                                                                                      776 ATCAGGCAGCAGGAGAGGCCAGTGCAGTTCTGGCGAAGGCCAAGGCTAAAGCTGAAGCTA 835
                                                                                                                                                                                                                           133 TGCCTCCAACCCTGGCGATGTCACCAGCATGGTGCAGCCATGGGTGTATATGGAG 74
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                                                                                                                                     Length 313;
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                                                                                      Sequence 313 BP; 60 A; 86 C; 89 G; 78 T; 0 other;
                                                                                                                                   Score 253; DB 22;
Pred. No. 4.6e-114;
0; Mismatches 1;
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breast cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 155; 297pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP
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ID AAS46972 standard; cDNA; 301
                                                                                                                                     21.3%;
llarity 99.7%;
Conservative (
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08-JUN-2000; 2000US-0590751.
22-JUN-2000; 2000US-0604287.
20-JUL-2000; 2000US-0620405.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-611721/70
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                                                                                                                                                          Similarity
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                                                                                                                                         Query Match
Best Local Simi
Matches 303;
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The invention relates to isolated breast tumour proteins and nucleic acids that encode them, including immunogenic fragments of the proteins. Also included are expression vectors expressing the proteins. Also included are expression vectors expressing the proteins or proteins, transformed cells and antibodies raised against the proteins or an antigen presenting cell expressing the protein. The proteins and nucleic acids may be used in the prevention, diagnosts and treatment of diseases associated with inappropriate breast tumour protein expression, i.e. breast tumours and breast cancer e.g by gene therapy. The nucleic acids and their complements may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. The proteins, nucleic acids and antibodies may be used in assays to identify modulators (e.g. antagonists) of breast tumour protein capression and activity. The antibodies may also be used to down regulate expression and activity. The antibodies may also be used to down regulate expression and activity. The antibodies may also be used to as diagnostic agents for detecting the presence of the proteins in samples (e.g. by enzyme linked immunosorbant assay (ELISA)) and in other immuno-purification diagnostic techniques. The present sequence is considered by subtractive.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hybridisation against a normal breast cona Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 301 BP; 48 A; 96 C; 72 G; 85 T; 0 other;
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Pred. No. 1.4e-112;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21.0%;
99.7%;
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Best Local Similarity 99.77
Watches 300; Conservative
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Human; breast cancer associated gene; vaccine; diagnosis; therapy; ss.
                                                           Human breast cancer associated JBTT21 coding sequence.
      AAF17542 standard; cDNA; 301 BP.
                                           (first entry)
                                                                                                                 WO200060076-A2
                                          13-MAR-2001
                                                                                                Homo sapiens
                                                                                                                                  12-OCT-2000.
                         AAF17542;
AAF17542/C
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15-FEB-2000; 2000WO-US05308

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of
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                                                                                                                                                                                                                                The present invention provides the coding sequences and some protein sequences of proteins associated with breast cancer in humans. These sequences can be used in the diagnosis and treatment of cancers,
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                                                                                                                                                     polypeptide useful for the treatment and diagnosis of breast cancer comprises at least an immunogenic portion
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Pred. No. 1.4e-112;
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Job time: 4267 sec
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99US-0339338.
99US-0389681.
99US-0433826.
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02-SEP-1999;
03-NOV-1999;
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/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
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/cgn2_6/ptodata/1/ina/Pcxfiles1.seq:*
                                             Compugen Ltd
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US-08-457-342-6
US-08-458-0768-6
US-08-47-338-4
US-08-47-338-4
US-08-764-2338-4
US-08-34-438-1
US-08-34-438-1
US-08-34-438-1
US-08-47-18-1
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US-08-48-10-38-34
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                   GenCore version
Copyright (c) 1993 - 2000
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    nucleic search, using sw model

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Gapop 60.0 , Gapext 60.0
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seq length: 2000000000
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Sequence 26, Appl
Sequence 32, Appl
Sequence 124, Appl
Sequence 23, Appl
Sequence 124, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 19, Appl
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Sequence 19, Appl
Sequence 1, Appli
Patent No. 5215895
Sequence 7, Appli
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Sequence 1
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Patent No. 5763589
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN MEMBRANE PROTEIN
UMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
US-08-480-547A-11
US-08-463-949A-11
US-08-464-410A-11
US-08-464-410A-11
US-08-76-259-26
US-08-814-095-7
US-08-814-095-7
US-08-994-031-32
US-08-994-131-124
US-08-998-416-992
US-08-118-111-19
US-08-118-111-19
US-08-017-52A-1
S-15895-2
US-08-017-52A-1
US-08-017-52A-1
US-08-017-52A-1
US-08-017-52A-1
US-08-017-52A-1
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MEDIUM TYPE: Diskette
COMPUTER: IBM COMPALIBLE
OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,562
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Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
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ATTORNEY/AGENT INFORMATION:
NAME: BIllings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: PE
TELECOMMUNICATION INFORMATION:
TELEPAN: 415-855
TELEPAX: 415-845-4166
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LENGTH: 1188 base pairs
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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TOPOLOGY: linear
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                                                                       APPLICANT: Ligon, James M.
APPLICANT: Ligon, James M.
APPLICANT: Beck, James Joseph
APPLICANT: Hill, Dwight Steven
APPLICANT: Ryals, John Andrew
APPLICANT: Gaffney, Thomas Deane
APPLICANT: Lam, Stephen Ting
APPLICANT: Hammer, Phillip E.
APPLICANT: Uknes, Scott Joseph
TITLE OF INVENTION: Genes for the synthesis of
TITLE OF INVENTION: antipathogenic substances
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
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REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: GGC 1506/CIP3
TELECOMUNICATION:
TELEPHONE: 919-541-8614
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Pred. No.
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/457,205
FILING DATE: 01-JUN-1995 .
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/258,261
FILING DATE: 08-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                               ; Sequence 6, Application US/08258261B
; Patent No. 5639949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23859 GCGGGGTCGGCCGCGCTC 23879
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Conservative 0;
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                                                                                                                                                                                                                                                                        Schupp, Thomas
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS:
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OPERATING SYSTEM:
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Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hawthorne
                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  õ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS
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Length 28958;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,342
                                                                       APPLICANT: Gaffney, Thomas Deane
APPLICANT: Lam, Stephen Ting
APPLICANT: Hammer, Phillip E.
APPLICANT: Uknes, Scott Joseph
TITLE OF INVENTION: Genes for the synthesis of
TITLE OF INVENTION: antipathogenic substances
NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
. 0.46;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/457,342
FILING DATE: 01-UN-1995
CLASSIFICATION 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/457,205
FILING DATE: 01-UN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
                                                                                                                                                                                                                                                E: Ciba-Geigy Corporation 7 Skyline Drive
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Ligon, James M.
Beck, James Joseph
Hill, Dwight Steven
Ryals, John Andrew
Gaffney, Thomas Deane
                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5679560
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                   Beck, James Joseph
Hill, Dwight Steven
Ryals, John Andrew
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Best Local Similarity 100.0%; P
Matches 21; Conservative 0;
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8614
TELEFAX: 919-541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129 GCCGCGCTCCGGCGCCTC 149
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Hammer, Phillip E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
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INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 28958 base pairs
TYPE: nucleic acid
Ligon, James M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
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MEDIUM TYPE: Floppy of COMPUTER: IBM PC comp
                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                 STREET: 7 Skyllr
CITY: Hawthorne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Schupp
                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ANTI-SENSE: NO US-08-457-342-6
                                                                                                                                                                                                                                                                                                                                COUNTRY: US
ZIP: 10532
                                                                                                                                                                                                                                                    ADDRESSEE:
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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US-08-457-646A-6
                                                        APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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                                               APPLICANT: Beck, James M.

APPLICANT: Beck, James Joseph
APPLICANT: Hill, Dwight Steven
APPLICANT: Hill, Dwight Steven
APPLICANT: Ryals, John Andrew
APPLICANT: Gaffney, Thomas Deane
APPLICANT: Lam, Stephen Ting
APPLICANT: Hammer, Phillip E.
APPLICANT: Hammer, Phillip E.
APPLICANT: Hammer, Phillip E.
APPLICANT: Mres, Scott Joseph
TITLE OF INVENTION: Genes for the synthesis of
TITLE OF INVENTION: antipathogenic substances
NUMBER OF SEQUENCES: 22
CORRESPONDENCES: 22
CORRESPONDENCES: 22
CORRESPONDENCES: 25
CORRESPONDENCE ADDRESSE:
ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BLM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,837
FILING DATE: 01-JUN-1995
CLLSSTFICATION ADATA:
APPLICATION NUMBER: 08/457,205
FILING DATE: 01-JUN-1995
FILING DATE: 01-JUN-1995
FILING DATE: 01-JUN-1995
APPLICATION NUMBER: 08/258,261
FILING DATE: 08-Jun-1994
ATONNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: 36,129
REFERENCE/DOCKET NUMBER: 36,129
TELECOMMUNICATION INFORMATION:
TELEFRAX: 919-541-8614
TELEFRAX: 919-541-8619
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Patent No. 5662898
GENERAL INFORMATION:
APPLICANT: Schupp, Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db 23859 GCCGCGCTCCGGCCGCCCTC 23879
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 28958 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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US-08-456-837-6
                                US-08-456-837-6
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APPLICANT: Schupp, Thomas
APPLICANT: Beck, James J.
APPLICANT: Hill, Dwight S.
APPLICANT: Hill, Dwight S.
APPLICANT: Nyals, John A.
TITLE OF INVENTION: Genes For The Biosynthesis Of Soraphen NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clab-delay Corporation
STREET: 520 White Plains Road, P.O. Box 2005
CITY: Tarrytown
STREET: Naint S.
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                                                                                                        MEDIUM TYPE: FLOPY disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
CONFIGNATION SYSTEM:
PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,076A
FILING DATE: 01-JUN-1995
APPLICATION NUMBER: US/08/457,205
FILING DATE: 01-JUN-1995
APPLICATION NUMBER: 08/258,261
FILING DATE: 08-Jun-1994
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: GC 1506/CIP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8619
INFORMATION FOR SEQ 1D NO: 6:
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No. 0.46;
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100.0%; Pre
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; Patent No. 5716849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db 23859 GCCGCGCTCCGGCCGCGCTC 23879
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 28958 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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MEDIUM TYPE: Floppy
                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
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Best Local Similarity
Matches 21; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
         Hawthorne
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APPLICANT: Ligon,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2
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                                                 USA
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                                                                      10532
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US-08-458-076A-6
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                                                    COUNTRY:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATA:
APPLICATION NUMBER: US/08/457,646A
FILING DATE: 01-JUN-1995
CLASSIFICATION NUMBER: 08/258,261
FILING DATE: 01-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAMME: ELEMEY, James Scott
RECISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: 36,129
REFERENCE/DOCKET NUMBER: 36,129
REFERENCE/DOCKET NUMBER: GCG 1506/CIP3
TELEPHONE: 919-541-8614
TELEFRAX: 919-541-864
TELEFRAX: 919-541-864
TELEFRAX: 919-541-864
SEQUENCE CHARACTERISTICS:
LENGTH: 28958 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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APPLICANT: Lam, Stephen Ting
APPLICANT: Hammer, Phillip E.
APPLICANT: Uknes, Scott Joseph
TITLE OF INVENTION: Genes for the synthesis of
TITLE OF INVENTION: antipathogenic substances
NUMBER OF SEQUENCES: 22
APPLICANT: Uknes, Scott Joseph
TITLE OF INVENTION: Genes for the synthesis of
TITLE OF INVENTION: antipathogenic substances
TITLE OF INVENTION: antipathogenic substances
CORRESPONDENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSE: Clba-Gelgy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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Beck, James Joseph
Hill, Dwight Steven
Ryals, John Andrew
Gaffney, Thomas Deane
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Patent No. 5698425
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HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 2: CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Schupp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ANTI-SENSE:
US-08-457-646A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
APPLICANT:
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US-08-458-076A-6
                                                                                                                                                                            STATE: N
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-729-214-6
Sequence 6, Application US/08729214
Fatent No. 5817502
GENERAL INFORMATION:
APPLICANT: Ligon, James M.
APPLICANT: Hill, Dwight Steven
APPLICANT: Hammer, Phillip E.
APPLICANT: Wan Pee, Karl-Heinz
APPLICANT: Wan Pee, Karl-Heinz
APPLICANT: Wan Pee, Karl-Heinz
APPLICANT: Winner, Sabine
TITLE OF INVENTION: Genes for the synthesis of
TITLE OF INVENTION: antipathogenic substances
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
. 0.46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                  FILING DATE: 08-Jun-1994
TATOREY AGENT THORNATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
TERERENELSE/PORT NUMBER: CGC 1506/CIP3
TELECOMUNICATION INFORMATION:
TELEPHONE: 919-541-8614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGC 1506/CIP5
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Tarrytown YAATE: No Marke Plains Road
                                                                                                                                                                                                                                                                                                                                                                                                                                  1.8%; Scc.
100.0%; Pre
0;
                     08/258,261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db 23859 GCGGCGCTCCGGCCGCCTC 23879
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TELEPHONE: 919-541-8887
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  129 GCCGCGCTCCGGCCGCCTC 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: CG
                                                                                                                                                                                                                                                                                                                           DNA (genomic)
                                                                                                                                                           TELEPHONE: 919-541-8614
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                          28958 base pairs
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nucleic acid
01-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Meigs, J. Timothy REGISTRATION NUMBER: 38
                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                     single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                               TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 21; Conserv
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                                                                                                                                                                                                                                                                                 STRANDEDNESS:
TOPOLOGY: lin
MOLECULE TYPE:
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STRANDEDNESS:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10591
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US-08-457-335A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Schupp, Thomas
APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James M.
APPLICANT: Beck, James M.
APPLICANT: Beck, James Joseph
APPLICANT: Hill, Dwight Steven
APPLICANT: Gaffney, Thomas Deane
APPLICANT: Lam, Stephen Ting
APPLICANT: Hammer, Phillip E.
APPLICANT: Hammer, Phillip E.
APPLICANT: Genes, Scott Joseph
TITLE OF INVENTION: Genes for the synthesis of
TITLE OF INVENTION: antipathogenic substances
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/729,214
FILLING DATE: 09-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/258,261
FILLING DATE: 08-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Med.gs, J. Timochy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: 38,241
REFERENCE/POCKET NUMBER: 38,241
REJECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8689
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 28958 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUNKESSEE: Ciba-Geigy Corporation STREET: 7 Skyline Drive CITY: Hawthorne STATE: NY COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,335A
FILLIO DATE: 01-JUN-1995
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/457,205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Sorangium cellulosum
IMMEDIATE SOURCE:
CLONE: p98/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/08457335A Patent No. 5723759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 10532
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOC CURRENM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db 23859 GCGGGGTCCGGCCGCGCTC 23879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            129 GCCGCGCTCCGGCCGCCTC 149
                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Sorangium cellulo
                                                                                                                                                                                                                                                                                                                                                                                                          roPoloGY: linear
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Gaps

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Indels

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Pred. No. 0.46; ; Mismatches

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100.0%; P1.
                                                                                                                     Db 23859 GCGGGGTCCGGCCGCGCTC 23879
                                                                             129 GCGGGGCTCGGGCGGCCTC 149
                  Best Local Similarity 100.
Matches 21; Conservative
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OTHER INFORMATION:
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OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                    US-08-764-233A-1
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0
                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Ligon, James M.
APPLICANT: Hill, Dwight S.
APPLICANT: Hill, Dwight S.
APPLICANT: Hill, Dwight S.
APPLICANT: Hammer, Philip E.
APPLICANT: Nan Pee, Karl-Heinz
APPLICANT: Nan Pee, Karl-Heinz
APPLICANT: Noung, Thomas R.
TITLE OF INVENTION: Pyrrolnitrin Biosynthesis Genes and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6117670artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
                                                                                                                                                                                                        ;
0
                                                                                                                                                                1.8%; Score 21; DB 1; Length 28958;
100.0%; Pred. No. 0.46;
                                                                                                                                                                                                          Indels
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/028,934
                                                                                                                                                                               100.0%; Pred. ...
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/729,214
FILING DATE: 09-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/258,261
FILING DATE: 08-0VY-1994
ATONEY/AGENT INFORMATION:
NAME: Medigs, J. Timothy
REGISTRATION NUMBER: 38,241
                                                                                                                                                                                                                                                                         Db 23859 GCGGGCTCCGGCCGCGCTC 23879
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/09028934 Patent No. 6117670
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
~~weiffeR: IBM PC compatible
~~weiffeR: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: CG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
                                                                                                                                                                                                                                                    129 GCCGCGCTCCGGCCGCCTC 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 28958 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                  DNA (genomic)
                                                                                                                                                                                     Best Local Similarity 100.
Matches 21; Conservative
                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Ligon,
                                                                    g
                         TOPOLOGY: line
MOLECULE TYPE: I
HYPOTHETICAL: NO
                                                                                   , ANTI-SENSE: NO
US-08-729-214-6
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US-09-028-934-6
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US-09-028-934-6
                                                                                                                                                                       Query Match
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Length 28958;

1.8%; Score 21; DB 3;

Query Match

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19:-10:-704-7123A-1

19:-10:-704-7124A-1

10:-10:-704-7124A-1

10:-10:-704-7124A-1

10:-10:-704-7124A-1

10:-10:-704-7124A-1

10:-10:-7
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CHROMOSOME 22 INVOLVED IN RECURRENT CHROMOSOMAL TRANSLATIONS ASSOCIATED WITH THE DEVELOPMENT OF CANCEROUS TUMORS, AND NUCLEIC ACIDS OF FUSION RESULTING FROM SAID TRANSLOCATIONS
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Sequence 18, Application US/08437027

GENERAL INFORMATION:
APPLICANT: Landanyi, Marc
APPLICANT: Gerald, William
TITLE OF INVENTION: A DAGNOSTIC TEST FOR TEST FOR THE DESMOPLASTIC
TITLE OF INVENTION: SMALL ROUND CELL TUMOR
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & Dunham LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION: 514
PRIOR APPLICATION DATA
APPLICATION NUMBER: PCT/FR93/00494
FILING DATE: 19-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92/06123
FILING DATE: 20-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERNEK/POCKET NUMBER: 989.6121P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 18;
                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: AEDIT 1.0 DOS text editor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
                                                                                         NUMBER OF SEQUENCES: 129
CORRESSONDENCE ADDRESS:
ADDRESSEE: Weiser & Associates
STREET: 230 South Fifteenth Street
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/343,443B FILING DATE: 18-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.08; Fr.
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INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     358 AGGAGGCCTGGGTGGTGG 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           194 AGGAGGCCTGGGTGGTGG 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 2371 base pairs
                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: Z15 CT TELEPHONE: Z15-875-8394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid
EDNESS: double
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                                                                                                                                                   STREET: 230 CTTY: Philadelphia
      TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25..1992
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                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 18 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New York
                                                                                                                                                                                                                             USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
US-08-437-027-18/c
                                                                                                                                                                                                                                                  ZIP: 19102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
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US-08-343-443B-1
                                                                                                                                                                                                                             COUNTRY:
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                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: 19871..46318
OTHER INFORMATION: /product= "SorB"
OTHER INFORMATION: /note= "dene product is highly homologous to type I PKS genes
FEATURE:
OTHER INFORMATION: are known to be involved in the synthesis of polyketide OTHER INFORMATION: compounds."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Inote—"The protein encoded by the sorM gene is highly homologous to the methyltransferase from Streptomyces hygroscopicus that is involved in the synthesis of the polyketide rappamicin."
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/ENTION: NUCLEIC ACID CORRESPONDING TO A GENE OF
                                                                  NAME/KEY: misc_feature
LOCATION: 942..7115
OTHER INFORMATION: /product= "Module 1 of Sora"
                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: 13455..19616
OTHER INFORMATION: /product= "Module 3 of SorA"
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LOCATION: 19870..24556
OTHER INFORMATION: /product= "Module 1 of SorB'
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LOCATION: 40190..46318
OTHER INFORMATION: /product- "Module 5 of SorB"
                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: 7203..12884
OTHER INFORMATION: /product= "Module 2 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: 24638.30820
OTHER INFORMATION: /product= "Module 2 of
FEATURE:
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LOCATION: 35528..40114
OTHER INFORMATION: /product= "Module 4 of
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LOCATION: 30881..35446
OTHER INFORMATION: /product= "Module 3 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: 46651..47891
OTHER INFORMATION: /product= "Sorm"
OTHER INFORMATION: /note= "The prote
OTHER INFORMATION: homologous to the
OTHER INFORMATION: hygroscopicus tha
OTHER INFORMATION: pygroscopicus tha
US-08-764-233a-1
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Desmaze, Chantal
Melot, Thomas
Peter, Martine
Ploougastel, Beatrice
Thomas, Gilles
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Best Local Similarity
Matches 21; Conserv
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APPLICANT: Aurias,
APPLICANT: Delati
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APPLICATION DAME:
APPLICATION NUMBER:
CLASSIFICATION: 4.24
ATTORNEY AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4070US1
TELEPHONE: (212) 751% 6849
                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.4%; Score 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 34, Application US/08468570
Patent No. 5871962
GENERAL INFORMATION:
APPLICANT: BUKH, J., MILLER, R.H. AND
APPLICANT: PURCELL, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,570
FILING DATE: 6-JUN 1995
CLASSIFICATION: 429
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INDIVIDUAL ISOLATE:
US-086-428B-34
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MEDIUM TYPE: FLOPEN
COMPUTER: IBM PC CO
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Best Local Similarity
Matches 17; Conservati
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                                        TYPE: nucleic acid
STRANDEDNESS: sing
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INFORMATION FOR SEQ ID
SEQUENCE CHARACTERIST
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                      LENGTH: 576 base
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                                                                                 TOPOLOGY:
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ANINO ACID SEQUENCES OF THE ENVELOPE 1 GENE
OF 51 ISOLATES OF HEPATITIS C AND THE USE
OF REAGENTS DERIVED FROM THESE SEQUENCES IN
DIAGNOSTIC METHODS AND VACCINES
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                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,027
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INPORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 46416/JPW/CCA
TELECOMMULCATION:
TELECOMMULCATION:
TELECOMMULCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    red. No. 14;
Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: BUKH, J., MILLER, R.H. AND APPLICANT: PURCELL, R.H.
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FILING DATE: 29-JUN-1993
CLASSIFICATION: 435
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345 PARK AVENUE
                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 18: SEQUENCE CHARACTERISTICS: LENGTH: 2412 base pairs TYPE: nucleic acid STRANDEDNESS: single
COMPUTER: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MSTRARE: Patert
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OPERATING SYSTEM: PC-DOS/MS
SOFTWARE: WORDERFECT 5.1
CURRENT APPLICATION DATA:
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REFERENCE/DOCKET NUMBER: 20.
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TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
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COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
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ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             194 AGGAGGCCTGGGTGG 211
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Best Local Similarity 100.
Matches 18; Conservative
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TITLE OF INVENTION: OF R
TITLE OF INVENTION: OF R
TITLE OF INVENTION: OF R
NUMBER OF SEQUENCES: 159
CORRESPONDENCE ADDRESS:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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KEYWORDS
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ArCC/DCTD/DTP
CDNA Library Preparation: Life Technologies Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Comporation
Clone distribution: MGC clone distribution information car
found through the I.M.A.G.E. Consortium/LLNU
http://image.llnl.gov
Plate: LLAM12233 row: a column: 09
                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; V
Mammalla; Eutheria; Primates; Catarrhini;
1 (bases 1 to 1037)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                               BM471641 1037
AGENCOURT_6465267 NIH_MGC_72
5', mRNA sequence.
                                                                                               Unpublished (1999)
Contact: Robert Strausberg,
                                                                                                                                                                                               BM471641.1
EST.
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Catarrhini; Hominidae;
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/db_xref="taxon:9606"
/clone="IMAGE:5539088"
/clone=lib="NIH_MGC_72"
/tlssue_type="melanotic melanoma"
/tlssue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pcMV-SPORT6; Site_1: Nr
Site_2: Sali; Cloned unidirectionally. Primer: Olaverage insert size 2 kb. Library constructed by Technologies."
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602326409F1 NIH_MGC_91 Homo:
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               National Institutes of Health, Ma
Unpublished (1999)
Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 749)
NIH-MGC http://mgc.nci.nih.gov/.
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//db_xref="taxon:9606"
//db_xref="taxon:9606"
//clone="IMAGE:427787"
//clone_lib="NHH_MGC_91"
//tissue_type="adenocarcinoma, cell line"
//tab_host="DH10B (phage-resistant)"
//note="organ: prostate; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.4 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."
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National Institutes of Health, M
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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1. (bases 1 to 770)
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Plate: LLCM1808 row:
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                      e: LLCM1808 row: d column: quality sequence stop: 767. Location/Qualifiers
          /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4905945"
/clone_lib="NHI_MGC_17"
/clone_lib="NHI_MGC_17"
/tissue_type="rhabdomyosarcoma"
/tissue_type="rhabdomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/lab_nost="Organ: muscle; Vector: pOTBF; Site_1: EcoRI;
/note="Organ: muscle; Vector: pOTBF; Site_susing the
pirectionally cloned into EcoRI/XhoI sites using the
pirectionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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Query Match Best Local Similarity

> 45.48; 99.78;

Score Pred.

539; DB 10; No. 1.1e-260;

Length 770;

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AUTHORS
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Tissue
                NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                            Homo
                                                                                                              mRNA sequence.
BI838402
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603083364F1 NIH_MGC_120
                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Pred. No. 2.6e-270;
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Catarrhini; Hominidae
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/clone_lib="NIH_MGC_120"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11025 row: i column: 06
High quality sequence stop: 793.
Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                     /note-"Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.5 kb. Library prepared by Life Technologies."
                                                                                                                                                                                                                                                                                                                                                 Technologies.
                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:9606"
/clone="IMAGE:4997837"
/clone_lib="NIH_MGC_10"
/cell_line="MGC36"
                                                                                                                                                                                                                                                                                                                                                                                                                         /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Homo sapiens"
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Pred. No. 2.5e-275;
0; Mismatches 2;
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BE740453
BE740453.1 GI:
                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 660)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
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601595494F1 NIH_MGC_9 Homo
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.
Plate: LLCM814 row: k column: 23
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/tissue_type="ademocarcinoma cell line"
/tote="organ: ovary; Vector: poTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally
cloned into ECORI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Site=selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3949582"
/clone_lib="NIH_MGC_9"
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672; Conserv
                                                                                                                                           AGENCOURT_6479118
5', mRNA sequence.
BM476304
                             Unpublished (1999)
Contact: Robert Strausberg,
                                               1 (bases 1 to 1110)
NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, M
                                                                     Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 1110)
         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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http://image.llnl.gov
Plate: LLAMI2282 row: k column:
High quality sequence start: 8
High quality sequence stop: 678.
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/Clone_lib="NIH_MGC_88"
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/Lib_host="DH108 (phage-resistant)"
/note="Organ: small intestine; vector: pCMV-SPORT6;
Site_1: NotI; Site_2: SalI; Cloned unidirectionally;
oligo-dT primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
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Score 571; DB 10;
Pred. No. 8.4e-277;
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TCACCCAGCTAGCTCAAACAACCATGAGATCAGAGCTCGGCAAACTCTCTNTGGACAAAG 499
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BM461614 BM461614.1 GI:18510654
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM12137 row: n column: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC
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Location/Qualifiers
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/db_xref="taxon:9606"
/clone=_lib="NAGE:5501391"
/clone_lib="NH_MGC_67"
/tissue_type="retinoblastoma"
/tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/lab_host="Organ: eye; Vector: pCMV-SPORT6; Si
/note="Organ: eye; Vector: pCMV-SPORT6; Si
Site_2: SalI; Cloned unidirectionally. Pr
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603623541F1 NIH_MGC_40 Homo sapiens
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National Institutes of Health, Mammalian
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/note="Organ: prostate; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MCC Library."
                                                                                                                                                                                                                                                       /db_xref="taxon:9606"
/clone="IMAGE:5449259"
                                                                                                                                                                                                                                                                                                                Location/Qualifiers
1. .887
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                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 1053)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collect
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs r@mail.nih.gov
                                                                                                                                                                              5', mRNA sequence.
BM456748
                                                                                                                                                                                         AGENCOURT_6403923
5', mRNA sequence.
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 cDNA Library Preparation: Life cDNA Library Arrayed by: The I.
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                                             TCACCAAAGCCCCAGTGCCAGGGACTCCAGACTCACTCTCCAGTTGGGAGCAGCAGCAGAGTG
                                                                                            CCTCCAACCCTGGCGATGTCACCAGCATGGTGGCTCAGGCCATGGGTGTATATGGAGCCC
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            TCCAGGGTACAGATGCAAGT
                                                                                 CCTCCAACCCTGGCGATGTCACCAGCCATGGTTGGCCCATGGGTGTATATGGAGCCC
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Location/Qualifiers
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/db_xref="taxon:9606"
/clone=lib="NH_MGC_92"
/clone_lib="NH_MGC_92"
/tissue_type="embryonal carcinoma, cell line"
/tissue_type="embryonal carcinoma, cell line"
/lab_host="DH108 (phage-resistant)"
/note="Organ: testis; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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BM453159
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National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="MAGE:5529785"
/clone="ib="NIH_MGC_71"
/tissue_type="leiomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="organ: uterus; vector: pCMV-SPORT6; Site_1: Not Site_2: Sali; Cloned unidirectionally. Primer: Oligo Average insert size 2.1 kb."
a 298 c 279 g 225 t
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AGENCOURT_6402181 NIH_MGC_41
5', mRNA sequence.
BM423347
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLCM2017 row: b column: 20
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Tissue Procurement: DCTD/DTP
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National Institutes of Health, Mammalian
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                          Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

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/lab_host="bH10B (phage=resistant)"
/lab_host="bH10B (phage=resistant)"
/note="0rgan: skin; Vector: poTB7; Site_1: xhoI; Site_2:
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                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutheria; Primates; Catarrhin1; Hominidae; 1 (bases 1 to 849)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
Bp 191 91006 EVRY cedex - France
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segref@genoscope.cns.fr,
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     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CSODC005YF20"
/clone_lib="LTI_NFL003_NBC3"
/sex="male"
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/note-"Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: filang@lifetech.com URL: http://fulllength.invitrogen.com"
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/product="HSPC108"
/product="HSPC108"
/product="HSPC108"
/protein_id="AAF29073.1"
/protein_id="AAF29073.1"
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/translation="MRGSLLASGRACRASSGLPRNTVVLFVPQQEAWVVERMGRFHRI
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               TGGAGTCCTTTACCTGCGCATCATGGACCCTTACAAGGCAAGCTACGGTGTGGAGGACCC
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Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genoscope - Centre National de Se
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, V
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 935)
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//db_xref="taxon:9606"
//clone="CSODE007YE18"
//clone_lib="LTI FL002_PL1"
//lab_host="DH10B"
//note="Organ: placenta; Vector: pcMVSPORT 6; 1st strand //note="Organ: placenta; Vector: pcMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcMVSPORT 6 vector. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville , Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL: thtp://fulllength.invitrogen.com" 4 others
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                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
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Zhang,Q.H., Ye,M., Wu,X.Y., Ren,S.X., Zhao,M., Zhao,C.J., Fu,G.,
Shen,Y., Fan,H.Y., Lu,G., Zhong,M., Xu,X.R., Han,Z.G., Zhang,J.W.,
Tao,J., Huang,Q.H., Zhou,J., Hu,G.X., Gu,J., Chen,S.J. and Chen,Z.
Cloning and functional analysis of cDNAs with open reading frames
for 300 previously undefined genes expressed in CD34+ hematopoietic
stem/progenitor cells
                                                                    Submitted (23-JUN-1999) Shanghai Institute of Hematology, Shanghai Second Medical University, Rui-Jin Hospital, 197 Rui-Jin Road II, Shanghai 200025, P. R. China Location/Qualifiers
1. .1218
                                                                                                                                    3 (bases 1 to 1218)
Ye,M., Zhang,Q.H., Zhou,J.,
Fan,H.Y., Mao,Y.F., Dai,M.,
Direct Submission
                                                                                                                                                                                                                                                                         Genome Res. 10 (10), 1546-1560 (2000) 20499367
                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens HSPC108 mRNA, complete cds. AF161458 AF161458.1 GI:6841439
                                                                                                                                                                                              Z (bases 1 to 1218)

Ye,M., Zhang,Q.H., Zhou,J., Shen,Y., Wu,X.Y., Guan,Z.Q., Wa Fan,H.Y., Mao,Y.F., Dai,M., Huang,Q.H., Chen,S.J. and Chen, Fun,H.Y. Mao,Y.F., Dai,M., Edward from cd34+ stem cells
                                                                                                                                                                                          Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CBCAPB12"
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/tissue_type="blood"
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BB2573795
BB25658444
BB256584435
BB256584435
BH01522493
BH1522493
BH1522493
BH162105
BG112719
BM4684070808
BB1862105
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BG70808
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BG761709
BF344401
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BF275386
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Huang, Q.H., Chen, S.J. and
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BM459766 AGENCOURT
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BM045444 603623560
BE256589 601110447
BG684435 602363189
BH1522433 603175452
BM162105 6033691995
BG112719 602282282
BM468407 AGENCOURT
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BH552983 603193616
BM0568438 60382330
BE73424 601565428
BE297150 601177559
BF34498 601563428
BE297150 601147859
BF34497 60262333
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                                                                                                                                                              Wang, L.,
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; LENGTH: 563
; TYPE: DNA
; ORGANISM: Homo s
PCT-US01-43704-58
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SEQ ID NO 841
LENGTH: 504
TYPE: DNA
ORGANISM: Homo sapiens
PCT-US01-43704-841
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                                                     NUMBER OF SEQ ID NOS: 2606
SOFTWARE: Corixa Invention
SEQ ID NO 58
                                                                                                                                                                                                                                                                Sequence 58, Application PC/TUS0143704 GENERAL INFORMATION:
                                                                                                    APPLICANT: Corixa Corporation
APPLICANT: Stolk, John A.
APPLICANT: Xu, Jiangchun
APPLICANT: Chenault, Ruth A.
APPLICANT: Chenault, Ruth A.
APPLICANT: Meagher, Madelein Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.561PC
CURRENT APPLICATION NUMBER: PCT/US01/43704
CURRENT FILING DATE: 2001-11-19
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Best Local Similarity
Matches 502; Conserv
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              sapiens
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                                                                        Disclosure Database
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Pred. No. 5.2e-197;
0; Mismatches 2;
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Query Match

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Score

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actgctggggtatccgctgcct 523
                ACTGCTGGGGTATCCGCTGCCT 581
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Search completed: September 22, 2002, 18:19:49
Job time: 5451 sec

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GENERAL INFORMATION:
APPLICANT: Jiang, Yuqiu
APPLICANT: Harlocker, Susan L.
APPLICANT: Secrist, Heather
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: AND DIAGNOSIS OF COLON
FILE REFERENCE: 20121.52762
CURRENT APPLICATION NUMBER: US/10/146,502
CURRENT FILING DATE: 2002-05-14
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 193
LENGTH: 454
TYPE: DNA
CRGANIEM: Homo sapiens
US-10-146-502-193
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Best Local Similarity
Matches 454; Conserv
                                                                                                                                                                                                 Sequence 2995, Application US/10214403 GENERAL INFORMATION:
                                           APPLICANT: Lodes, Michael J.
APPLICANT: Secrist, Heather
APPLICANT: Carter, Darrick
APPLICANT: Fanger, Gary R.
APPLICANT: Smith, Carole L.
                                                                                                                              APPLICANT: Jiang, Yuqiu
APPLICANT: Chenault, Ru
APPLICANT: Xu, Jiangchu
APPLICANT: Indirias, Ca
TITLE
              APPLICANT:
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            Durham, Margarita Stolk, John A.
                                                                                                                                 Indirias, Carol Yoseph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38.2%; Score 454; DB 7; llarity 100.0%; Pred. No. 7e-224; Conservative 0; Mismatches 0
                                                                                                                                            Jiangchun
COMPOSITIONS AND
                                                                                                                                                                 Ruth A.
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PCT-US01-43704-841

PCT-US01-43704-841

Sequence 841, Application PC/TUS0143704

GENERAL INFORMATION:

APPLICANT: Corixa Corporation

APPLICANT: Xu, Jiangchun

APPLICANT: Xu, Jiangchun

APPLICANT: Meagher, Madellein Joy

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR

TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER

FILE REFERENCE: 210121.561PC

CURRENT APPLICATION NUMBER: PCT/US01/43704

CURRENT FILING DATE: 2001-11-19

NUMBER OF SEO ID NOS: 2606
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FILE REFERENCE: 20121.593C1
CURRENT APPLICATION NUMBER: US/10/214,403
CURRENT FILING DATE: 2002-08-06
NUMBER OF SEQ ID NOS: 3420
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2995
LENGTH: 550
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Best Local Similarity
Matches 503; Conserv
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LOCATION: 411
OTHER INFORMATION: n =
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ORGANISM: Homo sapiens
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Pred. No. 2.3e-223;
0; Mismatches 1;
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                                                                               AND METHODS FOR
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RESULT 11
PCT-US01-43704-1161/c
Sequence 1161, Application PC/:
GENERAL INFORMATION:
APPLICANT: Corixa Corporation
APPLICANT: Stolk, John A.
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Best Local Similarity 99.4%;
Matches 892; Conservative
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                                                                                        AGCATGGTGGCTCAGGCCATGGGTGTATATGGAGCCCTCACCAAAGCCCCAGTGCCAGGG 1041
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Pred No. 7.2e-285;
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Sequence
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APPLICANT: Xu, Jiangchun
APPLICANT: Chenault, Ruth A.
APPLICANT: Meagher, Madelein Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THE
TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.561PC
CURRENT APPLICATION NUMBER: PCT/US01/43704
CURRENT FILING DATE: 2001-11-19
NUMBER OF SEQ ID NOS: 2606
SOFTWARE: COTIXA Invention Disclosure Database
SEQ ID NO 1161
LENGTH: 622
TYVE: DNA
ORGANISM: Homo sapiéns
PATURE:
NAME/KEY: misc_feature
LOCATION: 615
COTIER INFORMATION: n = A,T,C or G
PCT-US01-43704-1161
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Local :
CTCCAAACTGG
                                                   AGTTCTGGCGAAGGCCAAGGCTAAAGCTGAAGCTATTCGAATCCTGGCTGCAGCTCTGAC
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99.7%;
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Application US/10146502

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APPLICANT: Xu, Yongyao
APPLICANT: Xu, Yongyao
APPLICANT: Wang, Youzhen
APPLICANT: Wang, Youzhen
APPLICANT: Wang, Youzhen
APPLICANT: Wang, Youzhen
ITITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, ANI
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PRI
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT FILING DATE: 2002-07-18
CURRENT FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2010-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13409
LENGTH: 1150
                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 9
US-10-198-846-13409
Company 13409, A
                                                          ; FEATURE:
, NAME/KEY: misc_feature
; LOCATION: 1149, 1150
; OTHER INFORMATION: n =
US-10-198-846-13409
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Query Match
Best Local Similarity
                                                                                                                                                  LENGTH: 11
TYPE: DNA
                                                                                                                                    ORGANISM: Homo sapiens
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APPLICANT: Liu, Jin
TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM
TITLE OF INVENTION: LIBRARIES
FILE REFERENCE: 20411-752CON1
CURRENT APPLICATION NUMBER: US/09/919,002
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: APPLICATION NUMBER: 09,
PRIOR FILING DATE: FILING DATE: 1999-07-22
PRIOR FILING DATE: FILING DATE: 1998-02-13
NUMBER OF SEQ ID NOS: 13203
NUMBER OF SEQ ID NOS: 13203
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Sequence 11863, Application US/09919002
GENERAL INFORMATION:
APPLICANT: Leshkowitz, Dena
APPLICANT: Liu, Jin
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                                                           SEQ ID NO 11863
LENGTH: 1309
-09-919-002-11863
                                                                                                   NUMBER OF SEQ ID N
SOFTWARE: FastSEQ
                   ORGANISM:
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CURRENT EILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: JP 199-248036
PRIOR FILLING DATE: 1999-07-29
PRIOR APPLICATION NUMBER: JP 1999-300253
PRIOR FILLING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: JP 2000-118776
PRIOR FILLING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: JP 2000-183767
PRIOR FILLING DATE: 2000-05-02
PRIOR FILLING DATE: 2000-05-09
PRIOR APPLICATION NUMBER: JP 2000-241899
PRIOR APPLICATION NUMBER: JP 2000-241899
PRIOR APPLICATION NUMBER: 60/159,590
PRIOR APPLICATION NUMBER: 60/183,322
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US-09-629-469A-11009
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11009
LENCTH: 1244
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TITLE OF INVENTION: PRIMERS FOR SYNTHESIZING FULL-LENGTH CDNA AND
FILE REFERENCE: 084335/0123
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              TGAAAGAGTCTATGCAGATGCAGGTGGAGGCAGAGCGGCGGAAACGGGCCACAGTTCTAG
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WAKAMATSU, AI
NAGAI, KEIICHI
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Pred. No. 0;
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Sequence 3468, Application US/09705256A
GENERAL INFORMATION:
APPLICANT: Ma, Xiao-Jun; Dotson, Stanton B.: Mon:
TITLE OF INVENTION: Tumor Associated Molecules (T)
TITLE OF INVENTION: and prevention of cancer
FILE REFERENCE: 3214
CURRENT APPLICATION NUMBER: US/09/705,256A
CURRENT FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: US 60/164,285
PRIOR TILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 8259
SEQ ID NO 3468
LENGTH: 1234
TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                      GGGTGGTGGAGCGAATGGGCCGATTCCACCGGATCCTGGAGCCTGGTTTGAACATCCTCA 262
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                                                          tgcgcatcatggacccttacaaggcaagctacggtgtggaggaccctgagtatgccgtca
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Pred. No. 0;
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LOCATION: (1322)
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NAME/KEY:
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OTHER INFORMATION:
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DR FILLING DATE: 1997-07-08
DR FILLING DATE: 1997-07-08
DR FILLING DATE: 1997-08-18
DR APPLICATION NUMBER: 60/058,665
DR FILING DATE: 1997-09-12
DR APPLICATION NUMBER: 60/058,668
DR FILING DATE: 1997-09-12
DR APPLICATION NUMBER: 60/058,669
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DR APPLICATION NUMBER: 60/058,750
DR APPLICATION NUMBER: 60/058,750
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APPLICATION NUMBER: 60/1
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TH: 1322
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FILING DATE: 1997-10-02
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APPLICANT:
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YAMAMOTO, JUNIO ISHII, SHIZUKO HAYASHI, KOJ SAITO, KAORU

JUNICHI

US-09-629-469A-11009; Sequence 11009, Application; GENERAL INFORMATION:

US/09629469A

APPLICANT: OTA, TOSHIO APPLICANT: ISOGAI, TAI

ISOGAI, TAKAO NISHIKAWA, TETSUO HAYASHI, KOJI

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                                     TCCAAACTGGCCAAGGACTCCAACACTATCCTACTGCCCTCCAACCCTGGCGATGTCACC
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APPLICANT: Automorphic Applicant: Automorphic Applicant: Ren, Feiyan APPLICANT: Ma, Yunging APPLICANT: Zhao, Oing A. APPLICANT: Zhao, Oing A. APPLICANT: Zhao, Oing A. APPLICANT: Zhao, Oing A. APPLICANT: Yang, Yonghong APPLICANT: Dramanc, Radoje T. TITLE OF INVENTION: Novel Nucleic Acids and TITLE OF INVENTION: Novel Nucleic Acids and TITLE OF INVENTION NUMBER: US/10/119,428 CURRENT APPLICATION NUMBER: 09/596,193 PRIOR APPLICATION NUMBER: 09/596,193 PRIOR APPLICATION NUMBER: 09/574,454 PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: 09/579,705 PRIOR APPLICATION NUMBER: 09/519,705 PRIOR APPLICATION NUMBER: 09/519,705 PRIOR FILING DATE: 2000-03-07 NUMBER OF SEQ ID NO 37
LEGGTH: 9098
TYPE: DNA
ORGANISM: Homo Sapiens
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US-10-119-428-37
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GEMERAL INFORMATION:
APPLICANT: Tang, Y. T
APPLICANT: Liu, Chen
APPLICANT: Liu, Chen
APPLICANT: Wu, Chon
APPLICANT: Wehrman,
APPLICANT: Ren, Feiy
APPLICANT: Wa, Yunqi
APPLICANT: Zhou, Pin
APPLICANT: Zhou, Pin
APPLICANT: Zhoo, Qin
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Matches 957; Conserv
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Asundi, Vinod
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Wehrman, Tom
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TITLE OF INVENTION: 86 Human Secreted Proteing the File Reference: p2008plc1
CURRENT APPLICATION NUMBER: US/10/219,793
CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: 09/209,462
PRIOR FILING DATE: 1998-12-11
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/049,547
PRIOR FILING DATE: 1997-06-13
PRIOR APPLICATION NUMBER: 60/049,549
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PRIOR APPLICATION NUMBER: 60/049,566
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PRIOR APPLICATION NUMBER: 60/049,566
PRIOR FILING DATE: 1997-06-13
PRIOR APPLICATION NUMBER: 60/049,606
PRIOR FILING DATE: 1997-06-13
PRIOR PRIOR PRIOR DATE: 1997-06-13
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RESULT 4
US-10-198-846-12975
; Sequence 12975, Application
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
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APPLICANT: Xu, Yongyao
APPLICANT: Wang, Youzhen
APPLICANT: Wang, Youzhen
APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS,
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT,
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT FILING DATE: 2002-07-18
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1, 2, 1909, 19
; OTHER INFORMATION: n = 1
US-10-198-846-12975
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; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSEQ for Windows Version 4.
; SEQ ID NO 12975
; LENGTH: 1910
; TYPE: DNA
; ORGANISM: Homo sapiens
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TCTCCAAACTGGCCAAGGACTCCAACACTATCCTACTGCCCTCCAACCCTGGCGATGTCA
                                               CACAACATAATGGAGATGCAGCAGCTTCACTGACTGTGGCCGAGCAGTATGTCAGCGCGT
                                                                                             CAGTTCTGGCGAAGGCCAAGGCTAAAGCTGAAGCTATTCGAATCCTGGCTGCAGCTCTGA
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                                    cacaacataatggagatgcagcagcttcactgactgtggccgagcagtatgtcagcgcgt
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PRIOR FILING DATE: 1997-10-02
PRIOR APPLICATION NUMBER: 60/060,865
PRIOR FILING DATE: 1997-10-02
PRIOR APPLICATION NUMBER: 60/061,059
PRIOR FILING DATE: 1997-10-02
PRIOR FILING DATE: 1997-10-02
PRIOR FILING DATE: 1997-10-02
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NAME/KEY: SITE
NAME/KEY: (1337)
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LOCATION: (1335)
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                                                                 TGAAAGAGTCTATGCAGATGCAGGTGGAGGCAGAGCGGCGGAAACGGGCCACAGTTCTAG
                                                                                                                                                                                  TCTTCCGGGAACGGGAGTCCCTGAATGCCAGCATTGTGGATGCCATCAACCAAGCTGCTG
                                                                                                                                                                                                                                        TCACCCAGCTAGCTCAAACAACCATGAGATCAGAGCTCGGCAAACTCTCTTTTGGACAAG
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agtctgaggggacccgagagtcggccatcaatgtggcagaagggaagaaacaggcccaga
                                                                                                          actgctggggtatccgctgcctccgttatgagatcaaggatatccatgtgccaccccggg
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                                                    tgaaagagtctatgcagatgcaggtggaggcagagcggcggaaacgggccacagttctag
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; NAME/KEY: misc_feature
; LOCATION: 1841, 1842
; OTHER INFORMATION: n = A,T,C
US-09-785-276A-24973
                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/785,276A
CURRENT FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/18,319
PRIOR FILING DATE: 2000-02-17
PRIOR PLICATION NUMBER: 60/18,862
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR PILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 60/219,007
PRIOR APPLICATION NUMBER: 60/219,007
PRIOR APPLICATION NUMBER: 60/219,007
PRIOR APPLICATION NUMBER: 60/255,281
PRIOR FILING DATE: 2000-07-18
PRIOR FILING DATE: 2000-07-2-13
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SOFTWARE: FastSEQ for
SEQ ID NO 24973
LENGTH: 1842
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APPLICANT: Monahan, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: HUMAN PROSTATE CANCER
FILE REFERENCE: MRI-007B
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                                                                      GCCGCGCCTCTGGATTGCCCCGAAACACCGTGGTACTGTTCGTGCCGCAGCAGGAGG
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/cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
/cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
/cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
/cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
/cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
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/cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
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PCT-US01-43704-8841
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US-10-214-403-2995
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Sequence 5820, Ap	Sequence 30091, A	Sequence 6734, Ap	Sequence 7770, Ap	Sequence 14079, A	Sequence 7087, Ap	Sequence 26126, A	•	Sequence 9558, Ap	Sequence 12906, A	Sequence 16278, A	Sequence 596, App	Sequence 1950, Ap	Sequence 6996, Ap	Sequence 18465, A	Sequence 688, App	Sequence 21791, A	Sequence 15714, A	Sequence 26, Appl	Sequence 26, Appl

ALIGNMENTS

## ; LIBRARY: Consensus ; CLONE: Consensus ; SEQUENCE DESCRIPTION: SEQ ID US-09-898-216-2 RESULT 1 US-09-898-216-2 ; Sequence 2, Application US/09898216 ; GENERAL INFORMATION: ; GENERAL INFORMATION: TELEX: <Unknown> INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1188 base pairs TYPE: nucleic acid STRANDEDNESS: single APPLICATION NUMBER: 08/781,562 FILING DATE: <Unknown> ATTORNEY/AGENT INFORMATION: NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749 REFERENCE/DOCKET NUMBER: PF-01 COMPUTER: IBM COMPATIBLE OPERATING SYSTEM: DOS SOFTWARE: FESTSEM for Windows Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/898,216 FILING DATE: 02-Jul-2001 CLASSIFICATION: Unknown> IMMEDIATE SOURCE: TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555 TELEFAX: 415-845-4166 PRIOR APPLICATION DATA: COMPUTER READABLE FORM: MEDIUM TYPE: Diskette CORRESPONDENCE ADDRESS: ADDRESSEE: Incyte GOLI, Surya K. TITLE OF INVENTION: NOVEL NUMBER OF SEQUENCES: APPLICANT: Hillman, Jennifer L. STATE: CA COUNTRY: U CITY: Palo Alto ADDRESSEE: Incyte Pharmaceuticals, STREET: 3174 Porter Drive 94304 USA linear NOVEL HUMAN MEMBRANE PROTEIN NO: PF-0181 SD

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; FEATURE:
; NAME/KEY: nisc_feature
; LOCATION: (1296)...(264)
; OTHER INFORMATION: similar to gi2984585 in the genepept database release
; OTHER INFORMATION: Run with FASTXY 3.3t00, default parameters
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Best Local Similarity 99.8%;
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PRIOR FILING DATE: 1999-09-21
PRIOR APPLICATION NUMBER: US 09/465,877
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: NOT YET ASSIGNED PRIOR FILING DATE: 1999-01-19
NUMBER OF SEQ ID NOS: 10410
SOFTMARE: PLCT_genes Version 1.02
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TYPE: DNA
ORGANISM: Homo sapiens
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OR FILING DATE: 1999-04-15
OR APPLICATION NUMBER: US 09/274,861
OR APPLICATION NUMBER: US 09/274,861
OR APPLICATION NUMBER: US 60/125,453
OR APPLICATION NUMBER: US 60/126,605
OR APPLICATION NUMBER: US 60/126,605
OR FILING DATE: 1999-03-26
OR APPLICATION NUMBER: US 09/306,350
OR APPLICATION NUMBER: US 09/306,350
OR APPLICATION NUMBER: US 09/399,720
OR APPLICATION NUMBER: US 09/399,720
OR FILING DATE: 1999-09-21
OR PILING DATE: 1999-09-21
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ACCTGCGCATCATGGACCCTTACAAGGCAAGCTACGGTGTGGAGGACCCTGAGTATGCCG 439
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                                                              TCTTCCGGGAACGGGAGTCCCTGAATGCCAGCATTGTGGATGCCATCAACCAAGCTGCTG 559
                                                                                                                                                 TCACCCAGCTAGCTCAAACAACCATGAGATCAGAGCTCGGCAAACTCTCTNTGGACAAAG 499
                                                                                                                                                                                                 ACCTGCGCATCATGGACCCTTACAAGGCAAGCTACGGTGTGGAGGACCCTGAGTATGCCG 955
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Pred. No. 0;
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0 GGACTCCAGACTCACTCTCCAGTGGGAGCAGCAGAGATGTCCAGGGTACAGATGCAAGT 1098 	0 CCAGCATGGTGGCTCAGGCCATGGGTGTATATGGAGCCCTCACCAAAGCCCCAGTGCCAG 1039 	0 TCTCCAAACTGGCCAAGGACTCCAACACTATCCTACTGCCCTCCAACCCTGGCGATGTCA 979	O CACAACATAATGGAGATGCAGCAGCTTCACTGACTGTGGCCGAGCAGTATGTCAGCGGGT 919	0 CAGTTCTGGCGAAGGCCAAGGCTAAAGCTGAAGCTATTCGAATCCTGGCTGCAGCTCTGA 859 	0 TCCTGGCCTCCGAAGCAGAAAAGGCTGAACAGATAAATCAGGCAGCAGGAGAGAGGCCAGTG 799 	10 AGTCTGAGGGGACCCGAGAGTCGGCCATCAATGTGGCAGAAGGGAAGAAACAGGCCCAGA 739 	0 TGAAAGAGTCTATGCAGATGCAGGTGGAGGCAGAGCGGGCGG

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NAME/KEY: misc_feature

LOCATION: (1296)...(264)

OTHER INFORMATION: similar to gi2984585 in the genepept database release 114,

OTHER INFORMATION: Run with FASTXY 3.3t00, default parameters

US-09-471-275-865
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LENGTH: 1398
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EARLIER APPLICATION NUMBER: US 09/404,284
EARLIER FILING DATE: 1999-09-21
EARLIER APPLICATION NUMBER:
EARLIER FILING DATE: 1999-12-16
NUMBER OF SEQ ID NOS: 10451
NUMBER OF SEQ ID NOS: 10451
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ER APPLICATION NUMBER: US 09/274,861
ER FILING DATE: 1999-03-23
ER APPLICATION NUMBER: US 60/125,453
ER APPLICATION NUMBER: US 60/126,605
ER APPLICATION NUMBER: US 60/126,605
ER FILING DATE: 1999-03-26
ER FILING DATE: 1999-03-26
ER APPLICATION NUMBER: US 09/306,350
ER FILING DATE: 1999-05-07
ER APPLICATION NUMBER: US 09/399,720
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ER APPLICATION NUMBER: US 09.
ER FILING DATE: 1999-01-29
ER APPLICATION NUMBER: US 09.
ER FILING DATE: 1999-03-25
ER APPLICATION NUMBER: US 09.
ER FILING DATE: 1999-03-18
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ACCTGCGCATCATGGACCCTTACAAGGCAAGCTACGGTGTGGAGGACCCTGAGTATGCCG 439
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                                                            INFORMATION:
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                                                                      8410, Application US/09496914A
Drmanac,
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US-09-496-914A-8410/c
Sequence 8410, Application US/09496914A
GENERAL INFORMATION.
APPLICANT: Tang, Yuanhua T.
APPLICANT: Tillinghast, John
APPLICANT: Liu, Chenghua
APPLICANT: NOVEL CONTIGS Obtained
TITLE OF INVENTION: From Various Libraries
FILE REFERENCE: 787
CURRENT APPLICATION NUMBER: US/09/496,914A
CURRENT FILING DATE: 1990-07-14
CURRENT FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: US 09/353,690
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: US 09/45,400
PRIOR APPLICATION NUMBER: US 09/321,214
PRIOR FILING DATE: 1999-05-26
PRIOR APPLICATION NUMBER: US 09/31,517
PRIOR APPLICATION NUMBER: US 09/31,517
PRIOR APPLICATION NUMBER: US 09/31,517
PRIOR APPLICATION NUMBER: US 09/32,782
PRIOR APPLICATION NUMBER: US 09/32,611
PRIOR APPLICATION NUMBER: US 09/346,956
PRIOR FILING DATE: 1999-01-22
PRIOR FILING DATE: 1999-07-02
PRIOR PRIOR APPLICATION NUMBER: US 09/362,510
PRIOR PRIOR APPLICATION NUMBER: US 09/362,510

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CURRENT APPLICATION NUMBER: PCT/USO1/04098A
CURRENT FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: Not Yet Assigned
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 09/728,422
PRIOR APPLICATION NUMBER: 09/63,325
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 09/63,561
PRIOR FILING DATE: 2000-09-15
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 09/654,936
PRIOR APPLICATION NUMBER: 09/650,325
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 09/620,325
PRIOR FILING DATE: 2000-07-19
PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/598,075
PRIOR APPLICATION NUMBER: 09/598,075
PRIOR APPLICATION NUMBER: 09/560,875
PRIOR APPLICATION NUMBER: 09/560,875
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 3960
SOSTWARE: Custom
SEQ ID NO 2212
LENGTH: 1398
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PCT-US01-04098A-2212/c
                                                                                                                                   ; LENGTH: 1398
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US01-04098A-2212
                                                         Query Match
Best Local S
Matches 957
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TITLE OF IN
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GGACTCCAGACTCACTCTCCAGTGGGAGCAGCAGAGATGTCCAGGGTACAGATGCAAGT
                            GCCGCGCCTCTGGATTGCCCCGAAACACCGTGGTACTGTTCGTGCCGCAGCAGGAGG
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                                                         Conservative
                                                                        72.18;
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                                                                        Score
Pred.
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نام. 0;
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Sequence 865, Application US/09471
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hysed, Inc.
TITLE OF INVENTION: Novel Contigs
'TITLE OF INVENTION: From Various
FILE REFERENCE: 782
CURRENT APPLICATION NUMBER: US/05
CURRENT FILING DATE: 1999-12-23
EARLLER APPLICATION NUMBER: US 05

l Contigs Obtained Various Libraries

US/09/471 09/235

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US/09471275

RESULT 14 US-09-471-275-865/c

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GGACTCCAGACTCACTCTCCAGTGGGAGCAGCAGAGATGTCCAGGGTACAGATGCAAGT 1098
                               TCTCCAAACTGGCCAAGGACTCCAACACTATCCTACTGCCCTCCAACCCTGGCGATGTCA 979
                                                                                                CACAACATAATGGAGATGCAGCAGCTTCACTGACTGTGGCCGAGCAGTATGTCAGCGCGT
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CURRENT FILING DATE: 2001-03-13;
PRIOR APPLICATION NUMBER: US 09/338,467;
PRIOR FILING DATE: 1999-06-22;
PRIOR FILING DATE: 1998-06-22;
NUMBER OF SEQ ID NOS: 1022;
SOFTMARE: FRASTSEQ for Windows Version 4.0;
SEQ ID NO 941;
LENGTH: 1384;
TYPE: DNA
ORGANISM: Homo sapiens
US-09-808-384-941
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Pred. No. 0;
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PRIOR APPLICATION NUMBER: 09/560,875
PRIOR EILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 2700
SOFTWARE: CUSTOM
SEQ ID NO 1001
LENGTH: 1398
TYPE: DNA
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; Sequence 1001, Application PC/TUS0103800A
; GENERAL INFORMATION:
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Best Local :
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APPLICANT: Tang, Y, Tom et al
TITLE OF INVENTION: Novel Nucleic Acids and
FILE REFERENCE: 21272-030
CURRENT APPLICATION NUMBER: PCT/US01/03800A
CURRENT FILING DATE: 2001-02-05
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FILE REFERENCE: 1600.1193-001
CURRENT APPLICATION NUMBER: US/09/652,914
CURRENT FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/152,112
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 9677
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7997
LENGTH: 1384
TYPE: DNA
ORGANISM: Homo Sapiens
US-09-652-914-7997
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                                  Query Match
Best Local Similarity
Matches 957; Conserv
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TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES
TITLE OF INVENTION: THEREFOR
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GCCGCGCCTCCTCTGGATTGCCCCGAAACACCGTGGTACTGTTCGTGCCGCAGCAGGAGG
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                                    Conservative
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Mismatches
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US-09-808-384-941

Sequence 941, Application US/09808384
GENERAL INFORMATION:
APPLICANT: Gearing, David P.
APPLICANT: HOLTZMAN, Douglas A.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED
TITLE OF INVENTION: HUMAN PROSTATE STROMAL LIBRARY
FILE REFERENCE: 1600.1025-002
CURRENT APPLICATION NUMBER: US/09/808,384

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                                                 ccagcatggtggctcaggccatgggtgtatatggagccctcaccaaagccccagtgccag
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Sequence 7419, Application US/09652816
GENERAL INFORMATION:
APPLICANT: GULTIEREZ-Ramos, JOSE-CATIOS
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLE
TITLE OF INVENTION: THEREFOR
FILLE REFERENCE: 1600.1177-001
CURRENT APPLICATION NUMBER: US/09/652,816
CURRENT FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 06/152,111
PRIOR APPLICATION NUMBER: 06/152,111
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 9647
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7419
LENGTH: 1384
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US-09-652-816-7419
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                                                                                                            TCTTCCGGGAACGGGAGTCCCTGAATGCCAGCATTGTGGATGCCATCAACCAAGCTGCTG
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                                                actgctggggtatccgctgcctccgttatgagatcaaggatatccatgtgccaccccggg
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; LENGTH: 1384
; TYPE: DNA
; ORGANISM: HOMO :
US-09-652-913-8809
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TITLE OF INVENTION: NOVEL NUCLEIC ACID MOI
TITLE OF INVENTION: HEREFOR
FILE REFERENCE: 1600.1174-001
CURRENT APPLICATION NUMBER: US/09/652,913
CURRENT FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/152,107
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEO ID NOS: 10833
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8809
LENGTH: 1384
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99.8%; Pred. No. 0;
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RESULT 7
US 09-652-127-7358
; Sequence 7358, Applic
; GENERAL INFORMATION:
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CURRENT APPLICATION UMBER: US/09/652,12:
CURRENT FILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: 60/151,134
PRIOR FILING DATE: 1999-08-30
NUMBER OF SEQ ID NOS: 10475
SOFTWARE: FastSEQ for Windows Version 4
SEQ ID NO 7358
LENGTH: 1384
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Best Local Similarity
Matches 957; Conser
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ORGANISM: Homo
-09-652-127-7358
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APPLICANT: Shyjan, Andrew W.
APPLICANT: Richardson, Jennifer
APPLICANT: Holtzman, Douglas A.
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.1181-001
CURRENT APPLICATION NUMBER: US/09/649,162
CURRENT FILING DATE: 2000-08-28
PRIOR APPLICATION NUMBER: 60/151,057
PRIOR APPLICATION NUMBER: 60/151,057
PRIOR FILING DATE: 1999-08-27
NUMBER OF SEQ ID NOS: 9990
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7309
LENGTH: 1384
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; ORGANISM: Homo sapiens
US-09-649-162-7309
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Best Local Similarity
Matches 957; Conserv
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                 TGCCTGAGCAGTCGGCTGTGACTCTCGACAATGTAACTCTGCAAATCGATGGAGTCCTTT
                                                                 TCATCCCTGTGTTAGACCGGATCCGATATGTGCAGAGGTCTCAAGGAAATTGTCATCAACG
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                                              tcatccctgtgttagaccggatccgatatgtgcagagtctcaaggaaattgtcatcaacg
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Pred. No. 0;
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; Sequence 7925, Application US/09652109
; GENERAL INFORMATION:
APPLICANT: MCCARTHY, Sean A.

FITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND TITLE OF INVENTION: THEREFOR

FILE REFERENCE: 1600.1180-001
; CURRENT APPLICATION NUMBER: US/09/652,109
; CURRENT FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/151,128
pRIOR APPLICATION NUMBER: 60/151,128
pRIOR FILING DATE: 1999-08-30
NUMBER OF SCO ID NOS: 10105
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7925
; ORGANISM: HOMO US-09-652-109-7925
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TYPE: DN
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Matches 957; Conser
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CURRENT FILING DATE: 1999-66-22
EARLIER APPLICATION NUMBER: 60/090,177
EARLIER FILING DATE: 1998-06-22
NUMBER OF SEQ ID NOS: 1022
SOFTWARE: FastSEQ for Windows Version 3.0
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            TCTCCAAACTGGCCAAGGACTCCAACACTATCCTACTGCCCTCCAACCCTGGCGATGTCA
                                    cacaacataatggagatgcagcatcactgactgtggccgagcagtatgtcagcgcgt
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nilarity 99.88;
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; ORGANISM: HOMO
US-09-644-869-8024
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APPLICANT: McCarthy, Sean A.
APPLICANT: Holtzman, Douglas A.
APPLICANT: Holtzman, John
APPLICANT: Monahan, John
APPLICANT: Monahan, John
APPLICANT: Nover NOVER NOUTE TITLE OF INVENTION: NOVER NOVER OF INTELE OF INVENTION: THEREFOR FILE REFERENCE: 1600.1182-001
CURRENT APPLICATION NUMBER: US/09/644,869
CURRENT APPLICATION NUMBER: US/09/644,869
CURRENT FILING DATE: 2000-08-28
PRIOR APPLICATION UMBER: 60/151,062
PRIOR FILING DATE: 1999-08-27
NUMBER OF SEQ ID NOS: 9708
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TYPE: DNA
ORGANISM: HOMO
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                                                    ACTGCTGGGGTATCCGCTGCCTNCGTTATGAGATCAAGGATATCCATGTGCCACCCCGG
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TGAAAGAGTCTATGCAGATGCAGGTGGAGGCAGAGCGGCGGAAACGGGCCACAGTTCTAG
                                 actgctggggtatccgctgcctccgttatgagatcaaggatatccatgtgccaccccggg
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SOFTWARE: Patentl
SEQ ID NO 45
LENGTH: 1337
TYPE: DNA
                                                             OTHER INFORMATION: I
NAME/KEY: SITE
LOCATION: (1336)
OTHER INFORMATION: I
NAME/KEY: SITE
LOCATION: (1337)
OTHER INFORMATION: I
S-09-209-462B-45
   Query Match
Best Local Similarity
Matches 957; Conserv
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                                                                                                                                                                       ORGANISM: Homo sapiens FEATURE: NAME/KEY: SITE
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DR EFLING DATE: 1997-10-02
DR FILING DATE: 1997-10-02
OR APPLICATION NUMBER: 60/06
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FILING DATE: 1997-10-02
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APPLICATION NUMBER: 60/0
APPLICATION 1997-09-12
60/
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APPLICATION NUMBER: 60/058,668
APPLICATION 1997-09-12
ANTE: 1997-09-12
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FILING DATE: 1997-08-18
APPLICATION NUMBER: 60/C
FILING DATE: 1997-09-12
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APPLICATION NUMBER: 60/051,919
FILING DATE: 1997-07-08
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APPLICATION NUMBER: 60/052,989
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      Conservative
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Sequence 941, Application US/09338467
GENERAL INFORMATION:
APPLICANT: Gearing, David P.
APPLICANT: Holtzman, Douglas A.
APPLICANT: Holtzman, Douglas A.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES
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499 511 439

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REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PZ00)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEPHONE: (301) 309-8439
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 137 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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Matches 957
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MEDIUM TYPE: Diskette, 3
COMPUTER: HP VECLTA 486,
OPERATING SYSTEM: MSDOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: 86 Human Secreted Proteins NUMBER OF SEQUENCES: 318
                                                                                                                                                                                                               FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                       PRIOR APPLICATION DATA: APPLICATION NUMBER:
  212
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6 US-60-172-373-10483
5 US-60-164-285-3468
US-9-978-134-349
7 US-10-033-356-349
7 US-09-359-922-11863
7 US-09-959-928-11863
6 US-09-98-598-1161
3 US-09-98-598-1161
3 US-09-98-598-1161
7 US-10-046-935-193
7 US-10-081-124-244
5 US-09-652-127-341
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Sequence 45, Application US/09209462B

Sequence 45, Application US/09209462B

Sequence 45, Application US/09209462B

GENERAL INFORMATION:

APPLICANT: ROSen et al.

TITLE OF INVENTION: 86 Human Secreted Proteins

FILE REFERENCE: P2008P1

CURRENT FILING DATE: 198-12-11

PRIOR APPLICATION NUMBER: PCT/US98/12125

PRIOR APPLICATION NUMBER: 60/049,547

PRIOR FILING DATE: 1997-06-13

PRIOR FILING DATE: 1997-06-13

PRIOR FILING DATE: 1997-06-13

PRIOR APPLICATION NUMBER: 60/049,548

PRIOR FILING DATE: 1997-06-13

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Post-processing: Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Contact: MGC help desk
Email: cgapbs-femail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clone distribution: MGC clone distribution through the I.M.A.G.E. Consortium/LLNL at: Series: IRAL Plate: 5 Row: m Column: 8 This clone was selected for for form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: nisc_mgc@nhgri.nih.gov
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brook
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legasy
Lin,M., Maduro,O.L., Masiello,C., Mastrian,S.D., McCloskey,J.C
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.
Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.
Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (05-FEB-2001) National Institutes of Health, National Center Collection (MGC), Cancer Genomics Office, National Institute, 31 Center Drive, Room 11A03, Bethesda, MD 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HOMO sapiens, complete cds.
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/Product-"stomatin-like 2"
/rtanslation-"mLarapargTGALLLRGSLLASGRAPRRASSGLPRNTVVLFVPQQ
/rtanslation-"MLARAPARGTGALLLRGSLLASGRAPTLDNVTLQID
GVLYLRIMDPYKASYGVEDPEYAVTQLAQOTMRSELGKLSLDKVFRERESLINASIVDA
INQAADCWGIRCCLRYEIKDIHVPRVKESMQMOYEAERRKRATVLESEGTRESAINA
EGKKQAQILASEAEKAEQINQAAGEASAVLAKAKAKAEAIRILAAALTQHNGDAAASL
GYVAEQYVSAFSKLAKDSNTILLPSNPGDVTSMVAQAMGVYGALTKAPVPGTPDSLSSG
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                                                                                                                                                                                                                                             /note="Vector: pOTB7"
47. .1117
                                                                                                                                                                                                                                                                                         /clone="MGC:1179 IMAGE:3346384"
/tissue_type="Skin, melanotic m
/clone_lib="NIH_MGC_20"
/lab_host="DH10B-R"
                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="LocusID:30968"
/db_xref="taxon:9606"
                                                                                                                                                                                                                        /codon_start=1
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Primates;
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2, clone MGC:1179 IMAGE:3346384, mRNA,
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Catarrhini; Hominidae
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: matched mRNA gi:
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Submitted (26-JUN-2000)
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A novel member of the STOMATIN/EPB72/mec-2 family,
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Mammalia; Eutheria;
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EGKKQAQILASEAEKAEQINQAAGEASAVLAKAKAKAEAIRILAAALTQHNGDAAASL
TVAEQYVSAESKLAKDSNTILLESNPGDVTSMVAQAMGVYGALTKAPVPGTPDSLSSG
SSRDVQGTDASALDEELDRVKMS"
1222. 1227.
                                                                    /product="stomatin-like protein 2"
/protein_id="AaF91466.1"
/protein_id="AaF91466.1"
/db_xref="GI:9652259"
/translation="MLARAARGTGALLLRGSLLASGRAPRRASSGLPRNTVVLFVPQQ
/translation="MLARAARGTGALLLRGSLLASGRAPRRASSGLPRNTVVLFVPQQ
ZEAWVVERMGRFHRILEFGLNILIPVLDRITVRSELGKLVINVPFQSAVTLDNVTLQID
GVLVLRIMDFYKASYCVEDPFYAVTQLAOTTWRSELGKLVINVFRERESLNASIUNA
INQAADCWGIRCLRYEIKDIHVPPRVKESMQMQVEAERRKRATVLESEGTRESAINVA
                                                                                                                                                                                                                                 /note="member of the stomatin/band7/EPB72/MEC2 family: similar to the predicted Caenorhabditis elegans protei F30A10.5, to Caenorhabditis elegans MEC-2, and to the
                                                                                                                                                                                                                                                                                                         /gene="SLP2"
35. .1105
                                                                                                                                                                                                                sapiens stomatin
                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="9"
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/dev_stage="fetus"
1. .1260
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Treutlein, H.R.,
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                                                                                                                                                                             CCGAAGCAGAAAAGGCTGAACAGATAAATCAGGCAGCAGGAGAGGCCAGTGCAGTTCTGG
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NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'-6 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isogai, T., Ota, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuk Nishikawa, T., Nagai, K., Sugano, S., Shiratori, A., Sudo, H., Wagatsuma, M., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Chiba, Y., Ishida, S., Murakawa, K., Sugawara, M., Takahashi, M., Chiba, Y., Ishida, S., Murakawa, K., Ono, Y., Takiguchi, S., Watanabe, S., Kimura, K., Murakami, K., Ishii, S., Kawai, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Ishii, S., Kawai, Y., Saito, K., Masuho, Y., Ninomiya, K. and Iwayana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          oligo capping; fis (full insert sequence).
Homo sapiens teratocarcinoma cell_line:NT2 cDNA to clone_lib:NT2RM1 clone:NT2RM1000080.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
2 (bases 1 to 1244)
Isogai, T. and Otsuki, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AK027405 1244 bp
Homo sapiens cDNA FLJ14499 fis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     University of Tokyo.
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                /protein_id="BAB55091.1"
/db_xref="GI:14042060"
/tabslation="MLARARGTGALLLRGSLLASGRAPRRASSGLPRNTVVLEVPQQ
/tabslation="MLARARGTGALLLRGSLLASGRAPRRASSGLPRNTVVLEVPQQ
EAWVVERMGREHRILEPGLNILIPVLDRIRYVQSLKEIVINVPEQSAVTLDNVTLQID
GVYYLRIMDFYKASYGVEDFEYAVTQLAQTTMRSELGKLSLDKVFRERSSLNASIVDA
INQAADCWGIRGCLRYEIKDIHVPFYKESMOWOVEABERKRATVLESEGTRESAINVA
INQAADCWGIRGCLRYEIKDIHVPFYKESMOWOVEABERKRATVLESEGTRESAINVA
EGKKQAQILASEAEKAEQINQAAGEASAVLAKAKAKARAEAIRILAAALTQHNGDAAASL
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TVAEQYVSAFSKLAKDSNTILLPSNPGDVTSMVAQAMGVYGALTKAPVPGTPDSLSSG
                                                                                                                                                                               /codon_start=1
                                                                                                                                                                                                       /note="unnamed
                                                                                                                                                                                                                                                                                               /clone_lib="NT2RM1"
                                                                                                                                                                                                                                                                                                                      /cell_type="teratocarcinoma"
                                                                                                                                                                                                                                                                                                                                            /clone="NT2RM1000080"
/cell_line="NT2"
                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:9606
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                                                                                                                                                                                                                             Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://lmage.linl.gov Series: IRAL Plate: 27 Row: d Column: 1
This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (02-JUL-2001) National Institutes of Headene Collection (MGC), Cancer Genomics Office, Natinstitute, 31 Center Drive, Room 11A03, Bethesda,
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Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Shevchenko,Y., Brooks,S.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkney,C., Brooks,S.,
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
Lim,M., Maduro,O.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. CODNA Sequencing by: National Institutes of Sequencing Center (NISC),
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plete cds.
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                                /tissue_type="Lung, small cell carcinoma"
/clone_lib="NHL_MGC_7"
/lab_host="DH10B-R"
                                                                                            /organism="Homo sapiens"
/db_xref="LocusID:30968"
/db_xref="taxon:9666"
/clone="MGC:19715 IMAGE:3534656"
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                                                         CCGAAGCAGAAAAGGCTGAACAGATAAATCAGGCAGCAGGAGAGAGGCCAGTGCAGTTCTGG
                                                                                                                     GGACCCGAGAGTCGGCCATCAATGTGGCAGAAGGGGAAGAAGAGGCCCAGATCCTGGCCT 748
                                                                                                                                                                CTATGCAGATGCAGGTGGAGGCAGAGCGGCGGAAACGGGCCACAGTTCTAGAGTCTGAGG 688
                                                                                                                                                                                                                          GTATCCGCTGCCTCCGTTATGAGATCAAGGATATCCATGTGCCACCCCGGGTGAAAGAGT
                                                                                                                                                                                                                                          GTATCCGCTGCCTNCGTTATGAGATCAAGGATATCCCATGTGCCACCCCGGGTGAAAGAGT
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                                          CCGAAGCAGAAAAGGCTGAACAGATAAATCAGGCAGCAGGAGAGGCCAGTGCAGTTCTGG
                                                                                                       AACGGGAGTCCCTGAATGCCAGCATTGTGGATGCCATCAACCAAGCTGCTGACTGCTGGG
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53; Conservative
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/protein_id="aAH10152".1"
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/translation="mLAR3ARCTGALLLRGSLLASGRAPRRASSGLPRNTVVLEVPQQ
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GVLYLRIMDPYKASYGVEDPEYAVTQPAQTTMRSELGKLSIJDKVFRERESLNASIVDA
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EGKKQAQILASEAEKAEQINQAAGEASAVLAKAKAEAIRILAAALTOHNGDAAASL
TVAEQYVSAFSKLAKDSNTILLPSNPGDVTSMVAQAMGVYGALTKAPVPGTPDSLSSG
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330 c 372 g 264 t
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99.4%;
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Pred. No. 2.9e-258;
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789

CGAAGGCCAAGGCTAAAGCTGAAGCTATTCGAATCCTGGCTGCAGCTCTGACACAACATA

848

FEATURES

passed

clone was selected for ful ed the following selection to protein

criteria:

Location/Qualifiers

/organism="Homo sapiens" /db\_xref="LocusID:30968"

Clone distribution: MGC clone distribution information can be through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gseries: IRAL Plate: 34 Row: p Column: 12
This clone was selected for full length sequencing because it

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Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
                                                                                                                                      cDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (01-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD:20892-2590,
                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                            NIH-MGC Project URL: h
Contact: MGC help desk
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Eutheria; Primates;
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/product="stomatin-like 2
/protein_id="AAH14990.1"
/db_xref="GI:15929070"
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/tissue_type="Pancreas, epithelioid
/clone_lib="NIH_MGC_42"
/lab_host="DH10B-R"
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Homo sapiens,
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           Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
                                                                                                                                            DNA Sequencing by
BC Cancer Agency,
info@bcgsc.bc.ca
                                                                                                                                                                             cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium DNA Sequencing by: Genome Sequence Centre,
                                                                                                                                                                                                                                 NIH-MGC Project URL: http://mgc.nci.nih.
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (06-FEB-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
Eukaryota; Metazoa;
Mammalia; Eutheria;
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Marco Marra.
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TCCGTTATGAGATCAAGGATATCCATGTGCCACCCCGGGTGAAAGAGTCTATGCAGATGC
                                      CTCTCGACAATGTAACTCTGCAAATCGATGGAGTCCTTTACCTGCGCATCATGGACCCTT
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EAMVVERWGREHRILEPGLNILLPVLDBIRYVQSLKEIVINVEDGSAVTLDNVTLQID
GVLYLRIMDPYKABSYGVEDPEYAVTQLAQTTMRSELGKLSLDKVFREERSLNASIVDA
INQAADCWGIRCLRYEIKDIHVPPRVKESMQMQYEAERRKRATVLESEGTRESAINVA
EGKKQAQILASEAEKAEDINQAAGEASAVLAKAKAKAEAIRILAAALTQHNGDAAASL
TVAEQYVSAFSKLAKDSNTILLESNPGDVTSMVAQAMGVYGALTKAPVPGTPDSLSSG
SSRDVQGTDASLDEELDBVKMS"
a 324 c 364 g '260 t
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23. .1093
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/product="stomatin-like;
/protein_id="AAH03025.1"
/db_xref="GI:12804333"
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/tissue_type="Lung, small cell
/clone_lib="NIH_MGC_7"
/lab_host="DH10B-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="LocusID:30968"
/db_xref="taxon:9606"
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1 (bases 1 to 1253)
Chang, J.G. and Chan, W.L.
Mouse stomatin-like protein
Unpublished
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Mus musculus stomatin-like
AF323178
AF323178.1 GI:12382776
                                                                                                                                                         Submitted (21-NOV-2000) Department of Medical Research, Medical College Hospital, 2, Yuh-Der Road, Taichung 404,
                                                                                                                                                                                                2 (bases 1 to 1253)
Chang, J.G. and Chan, W.L.
                                                                                                                                                                                        Direct Submission
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/product="stomatin-like
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                                                                 /tissue_type="kidney"
32. .1093
                                                                                                       /organism="Mus
/strain="FVB"
                                       /codon_start=1
                                                     /note="MSLP2"
                                                                                            /db_xref="taxon:10090"
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AGATGCAGCAGCTTCACTGACTGTGGCCGAGCAGTATGTCAGCGCGGTTCTCCCAAACTGGC
                                         GGCCAAGGCTAAAGCTGAAGCTATTCGAATCCTGGCTGCAGCTCTGACACAACATAATGG
                                                                                                  GCAGATGCAGGTGGAGGCAGAGCGGGCGGAAACGGGCCACAGTTCTAGAGTCTGAGGGGAC
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02; Conservative
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EAMVVERWGRFHRILEPGLNVLLFVLDRIRYVQSLKEIV INVPEQQSAVTLDNVTLQID
GVLVLRIMDPYKASYGVEEDPEAVTQLAQTTMRSELGKLSLDKVFREBESLANNIVDA
INQAADCWGIRCLRYEIKDIHVPPRVKESMQMQVEAERRKRATVLESEGTRESAINVA
EGKKQAQILASEAEKAEQINQAAGEASAVLAKAKAKAEAIRILAGALTQHNGDAAASL
TVAEQYVSAFSKLAKDSNTVLLPSNPSDVTSMVAQAMGVYGALTKAPVPGAQNSSQSR
RDVQATDTSIEELGRVKLS"
258 t
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Pred. No. 9.7e-196;
0; Mismatches 125;
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                                                                                                                                                                                                                                                                                                                Clone distribution: MGC clone distribution information can be fo
through the I.M.A.G.E. Consortium/LLML at: http://image.llnl.gov
Series: IRAK Plate: 5 Row: k Column: 5.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www.hgsc.bcm.tmc
Contact: villalon@bcm.tmc.edu.
Villalon, D.K., Luna, R.A., Hale,
A.M., Holloway, M., Telford, B, H
Muzny,D.M., Gibbs,R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium DNA Sequencing by: Baylor College of Medicine Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue procurement: Jeffrey Green M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BC003425 1565 bp n
Mus musculus, RIKEN cDNA 0610038F01
IMAGE:2609584, mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene Collection (MGC), Cancer Genomics Institute, 31 Center Drive, Room 11A03,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (20-FEB-2001) National Institutes of Health, Mammali Gene Collection (MGC), Cancer Genomics Office, National Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center code: BCM-HGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequencing Center
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                                                                                                                                                     /clone="MGC:6777 IMAGE:2609584"
/tissue_type="Mammary tumor. C3(1)-Tag model.
ductal carcinoma. 5 month old virgin mouse."
/clone_lib="NCI_CGAP_Mam6"
                /codon_start=1
/product="RIKEN CDNA 0610038F01
/protein_id="AAH03425.1"
/db_xref="GI:13097354"
                                                                                              /note="Vector: 12. .1073
translation="MLARAARGTGALLLRGSVQASGRVPRRASSGLPRNTVILFVPQQ/
                                                                                                                                       /lab_host="DH10B"
                                                                                                                                                                                                                                     /db_xref="LocusID:66592"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                            /organism="Mus musculus"
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Rodentia;
                                                                                                                  PCMV-SPORT6"
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GCTATTCGAATCCTGGCTGCAGCTCTGACACACATAATGGAGATGCAGCAGCTTCACTG
                                                                                                                                         ATAAATCAGGCAGCAGGAGAGGCCAGTGCAGTTCTGGCGAAGGCCAAGGCTAAAGCTGAA
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                                                              GCGATTCGAATTCTGGCTGGGGCTCTGACTCAACATAATGGAGATGCAGCAGCTTCGCTC
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INQAADCWGIRCLRYBIKDIHVPPRVKESMQMQVEAERRKRATVLESEGTRESAINVA
EGKKQAQILASEAEKAEQINQAAGEASAVLAKAKAEAIRILAGALTQHINGDAAASL
TVAEQYVSAFSKLAKDSNTVLLPSNPSDVTSMVAQAMGVYGALTKAPVPGAQNSSQSR
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Mammalia; Eutheria;
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  TCTTCCGGGAACGGGAGTCCCTGAATGCCAGCATTGTGGATGCCATCAACCAAGCTGCTG
                     ACCTGCGCATCATGGACCCTTACAAGGCAAGCTACGGTGTGGAGGACCCTGAGTATGCCG 439
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1 (bases 1 to 518)

Xu, J., Lodes, M.J., Secrist, H., Benson, D.R., Meagher, M.J., Stolk, J.A., King, G.E., Wang, T. and Jiang, Y.

Compounds for immunotherapy and diagnosis of colon cancer and methods for their use Patent: WO 0149716-A 1031 12-JUL-2001;

CORIXA CORPORATION (US)
LOCATION (US)
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         TCAGGCCATGGGTGTATATGGAGCCCTCACCAAAGCCCCAGTGCCAGGGACTCCAGACTC 1052
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jiang, Y., Harlocker, S.L. au
Compositions and methods fi
cancer
Patent: WO 0196388-A 193 2
CORIXA CORPORATION (US)
                                               CAAGGACTCCAACACTATCCTACTGCCCTCCAACCCTGGCGATGTCACCAGCATGGTGGC
                                                                                              AGATGCAGCAGCTTCACTGACTGTGGCCGAGCAGTATGTCAGCGCGTTCTCCAAACTGGC
                                                                                                                                             GGCCAAGGCTAAAGCTGAAGCTATTCGAATCCTGGCTGCAGCTCTGACACAACATAATGG
 TCAGGCCATGGGTGTATATGGAGCCCTCACCAAAGCCCCAGTGCCAGGGACTCCAGACTC
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AX339946
Sequence 193 from Patent
AX339946
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                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
123 c 137 g 7
                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1. .457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Harlocker, S.L.
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                                                                                                                                                                                                                                                                                                                                              38.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                   Score 455.2; DB Pred. No. 1e-97; 1; Mismatches
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WO0196388
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for
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the therap
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    VERSION
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                                                                                                Locus
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                193 CAGGAGGCCTGGGTGGAGCGAATGGGCCGATTCCACCGGATCCTGGAGC-CTGGTTT 251
                                                                                                                                                                                                                     485
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                                                                                                                                                                                                                  CNCCCCGGTGAAANA 499
                                                                                                                                                                                                                                                                                                                                                                                                     GTATGCCGTCACCCAGCTAGCTCAAACAACCATGAGATCAGAGCTCGGCALACTCTCTNT 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGTCCTTTACCTGCGCATCATGGACCCTTACAAGGCAAGCTACGGTGTGGAGGACCCTGA 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATCAACGTGCCTGAGCAGTCGGCTGTGACTCTCGACAGTGTAACTCTGCAAATCGATGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAACATCCTCATCCCTGTGTTAGACCGGATCCGATATGTGCAGAGTCTCAAGGAAATTGT 184
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                                                                                                                                                                                                                                                            ACCCCGGGTGAAAGA 626
                                                                                                                                                                                                                                                                                                              AGCTTCNTACTGTTNGGGNATCCCTTNCTCCGTTNTNAAAATAANNGATATCCATTNTNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTATGCCGTCACCCAGCTAGCTCAAACAACCATGANATCAGAGCTCGGCAAACTCTCTCT
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                                                                                                                                                                                                                                                                                                                                                             AGCTGCTGACTGCTGGGGTATCCGCTGCCTNCGTTATGAGATCAAGGATATCCATGTGCC
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AX260945
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AC095312
AC095312.2 GI:17943711
                                       Rattus norvegicus clone CH230-14D17,
***, 61 unordered pieces.
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                                                                                              AC095312
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596 from Patent WO0173027.
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/db_xref="taxon:9606"
181 c 169 g 15
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90.3%;
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Pred. No. 4.
                                                                                           186656 bp
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                                                                       SEQUENCING
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                                                                                              HTG 20-DEC-2001
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JOURNAL
REFERENCE
AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Burch, Burch, Burch, Burn, K.L. Byrd, N.C. Carron, T.F.
Carter, M. Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R.,
Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox.C.,
Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C.,
Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C.,
Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C.,
Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C.,
Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C.,
Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C.,
Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C.,
Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C.,
David, R., David, R., David, R., David, R., David, C.,
David, R., David, R., David, R., David, R., David, C.,
David, R., Hale, S., Hame, J., Hart, M., Havlak, P., Hawes, A.,
Herinandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C.,
Hollins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J.,
Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J.,
Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C.,
Li, J., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W.,
Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W.,
Lewis, L., Li, J., Li, Mapua, P., Wartin, R., Martindale, A.,
Martinez, E., Massey, E., Mawhiney, E., McLeoch, M., Mohabbat, K.,
Morgan, M., Morris, S., Moser, M., Neal, D., Newtson, J., Newtson, N.,
Nguyen, A., Nguyen, N., Nickerson, E., Nockenkwo, S.,
Oguh, M., Okwuonu, G., Oragunye, N., Ordedo, R., Pace, A., Payton, B.,
Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L. L.,
Oguh, M., Morris, S., Moser, M., Rojas, A., Rojas
                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (16-SEP-2001) Human Genome Sequencing Center, Depai of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA
On Dec 20, 2001 this sequence version replaced gi:15625866.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 186656) Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HTG; HTGS_PHASE1.
                                                                                                                                                              findPhrapList
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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            Consensus quality: 152607, bases at least Q40
Consensus quality: 159995 bases at least Q30
Consensus quality: 167102 bases at least Q20
Estimated insert size: 161475; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 2.2x in Q20 bases; sum-of-contigs estim
                                                                                                                                                                                  Center project name: GEHL
Center clone name: CH230-14D17
----- Summary Statistics
Assembly program: Phrap; version 0.990329First call
                                                                                                                                                                                                                                                                           Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a "working draft' sequence. It currently consists of 61 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Search completed: September 22, 2002, 15:23:13 Job time: 7259 sec

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Copyright (c) 1993 - 2000 Comp
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## RESULT AAV28867 03-AUG-1998 (first entry) AAV28867; AAV28867 standard; DNA; 1188 ВP

Human; integral membrane protein; IMP; cancer; anaemia; prostate, breast; pancreatic; tumour; ion transport; ss.

Human integral membrane protein encoding DNA.

09-JAN-1997; 09-JAN-1997; 09-JUN-1998 US5763589-A (INCY-) INCYTE PHARM INC Homo sapiens. 97US-0781562. 97US-0781562. /product= "integral membrane protein"
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Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
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The invention relates to 86 novel genes and their fragments (nucleic cid sequences: AAX04311-X04410; amino acid sequences AAW78126-W78225) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polynucleotides. Specific uses are described for each of the 86 polynucleotides, based on which tissues they are most highly expressed in (see AAX04311 for described uses).
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                    GCCTGGTTTGAACATCCTCATCCCTGTGTTAGACCGGATCCGATATGTGCAGAGTCTCAA
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Sequences ABB10981-ABB12330 represent nucleic acids encoding them. The cinvention also relates to vectors and recombinant host cells comprising a CC invention also relates to vectors and recombinant host cells comprising a CC antibodies against the polypeptides, methods of deecting the nucleotides, cc antibodies against the polypeptides, methods of deecting the nucleotides or polypeptides in a sample, and methods of identifying compounds which completely an insight into their probable biological activities, and hence compounds an insight into their probable biological activities, and hence compounds an insight into their probable biological activities, and hence compounds an insight into their probable biological activities, and hence compounds an insight into their probable biological activities, and hence compounds an insight into their probable biological activities, and hence compound an insight into their probable biological activities of the invention may be necessary activity; tissue growth factory activity. CC immunomodulatory activity; activity; tissue growth factory activity; change growth factory activity; change growth factory activity; changed activities; or may be convolved in oncogenesis, cancer cell proliferation or metastasis. CC conditions are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include conditions, include conditions, include conditions (e.g., asthma or arthritis), cc arterial ischaemia, bone disorders (e.g., myeloid or lymphoid cell conditions, conditions, conditions (e.g., asthma or arthritis), cc arterial and tungal infections in addition to immune disorders with growth factor activity may be used to promote wound conditions in addition to immune disorders.

CC manipulate stem cells in culture to give rise to neuropithelial cells caused to augment or replace cells damaged by illness,
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20-OCT-2000;
30-NOV-2000;
The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or
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                                                        This sequence represents a nucleic acid molecule which encodes a CC secreted human protein. The gene number, and the clone it is derived from, are detailed in the descriptor line. The gene can be used to CC from, are detailed in the descriptor line. The gene can be used to CC generate fusion proteins by linking to the gene to a human immunoglobulin FC portion (e.g. AAX04302) for increasing the stability of the fused CC protein as compared to the human protein only.

CC The invention relates to 86 novel genes and their fragments (nucleic acid sequences: AAX04311-X04410; amino acid sequences AAW78126-W78225)

CC which are useful for preventing, treating or ameliorating medical CC conditions e.g. by protein or gene therapy. Also, pathological CC conditions can be diagnosed by determining the presence of mutations in CC polypeptides in a sample or by determining the presence of mutations in CC polypuclasions of the new polynucleotides. Specific uses are described for each of the 86 cpolynucleotides, based on which tissues they are most highly expressed in CC (see AAX04311 for described uses).
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02-OCT-1997;
02-OCT-1997;
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CC full-length cDNAs defined in the specification. Where a primer set to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the configuration comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide which comprises as 5'-end sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the coligonucleotide comprises a 3'-end sequence, where the coligonucleotide comprises a 3'-end sequence, where the coligonucleotide comprises as 1 nucleotides and the combination of the specification. The primer sets can be used in antisense therapy and the specification. The primer sets can be used in antisense therapy and configuration and/or diagnosis of the primers are also useful for the detection and/or diagnosis of the primers are also useful for the combination of the full-length cDNAs. The primers are also useful for the full-length cDNAs and the specialised methods. AAH03166 to AAH13628 and CC anab35893 represent human amino acid sequences; and AAH13629 to AAH13632 represent human amino acid sequences; and AAH13629 to AAH13632 or represent oligonucleotides, all of which are used in the exemplification cc of the present invention
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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
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Human; secreted protein; arthritis; Crohn's disease; sepsis; shock; ischaemia-reperfusion injury; haematopoissis; cancer; neuropathy; transgenic animal; Alzheimer's disease; Parkinson's disease; burn; amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia; ulcer; osteoporosis; bone degenerative disorder; periodontal disease
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The invention relates to novel isolated human secreted polypeptides (I) CC and polynucleotides (II). (I) and (II) are useful for treating conditions such as arthritis, nephritis, Crohn's disease, ischaemia-reperfusion injury, shock, sepsis, immune responses, and is involved in increasing haematopoiesis, stem cell survival, bone growth CC and remodeling. (I), (II) and modulators of (II) are useful for CC prophylaxis or treatment of one or more cancers. (II) is also useful for CC the polypeptide as well as for studying modulators of the polypeptides. (II) induces the proliferation of neural cells and regeneration of nerve and brain tissue and is useful for the treatment of central and CC peripheral nervous system diseases and neuropathies, such as Alzheimer's, Parkinson's disease, Huntington's disease, and amyotrophic lateral CC sclerosis. In addition, (I) is involved in chemotactic or chemokinetic activity, regulation of haematopoiesis and is useful for treating myeloid CC or lymphoid cell disorders, platelet disorders such as thrombocytopenia and for regeneration of bone, cartilage, tendon, ligament and/or nerve culcers, for treating osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease. Furthermore, (I) is also useful for culcativity in various tissues, various immune deficiencies and CC fungal infections, autoimmune disorders e.g. multiple sclerosis, allerdic crhematoid arthritis, diabetes mellitus, myasthenia scravis, allerdic
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19-MAY-2000;
17-JUN-2000;
14-JUL-2000;
19-SEP-2000;
20-OCT-2000;
                               dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides analgesic effects or other pain reducing effects, immunoglobulin like activity and can act as an antigen in a vaccine composition to raise an immune response. AAS44920-AAS45295 represent novel human secreted protecoding sequences of the invention.
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                                                                                                                          rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic reactions and conditions, such as asthma or other respiratory problems: In addition, (I) affects biorhythms or circadian cycles of rhythms, fertility, metabolism, catabolism, anabolism, storage or elimination of fertility metabolism, catabolism, anabolism, storage or elimination of
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04-MAY-2000;
05-MAY-2000;
                                                                                                                                                                  Th present invention relates to the isolation of novel cDNA sequences encoding for at least an immunogenic portion of human colon tumour proteins. The sequences of the invention are useful in pharmaceutical compositions and vaccines for the prevention and treatment of cancers such as colon cancer. They are also useful for the diagnosis and monitoring of such cancers. Antibodies to the colon tumour proteins and antigen presenting cells that express polynucleotides encoding colon tumour proteins can be used to inhibit the development of cancers. T-cells that react specifically with colon tumour proteins are useful for removing tumour cells from samples (e.g. blood) and for cancer treatment. The polynucleotides sequences are also useful ir gene therapy. AAS57325-AAS5880 represent the cDNA sequences of the invention that encode for portions of human colon tumour proteins.
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    Example
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; 2000JP-0118774.
; 2000JP-0183765.
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                                                                                                                                                    Sugiyama
  ID NO
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1652; 1380pp + sequence listing;
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ı T, Nagai
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K, Kojima
                                                               full length
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                                                               cDNA clones
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  English
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RESULT 1 AAH05115 ID AAH(

AAH05115

standard; cDNA;

567

XEXEXX

26-JUN-2001 (first entry)
Human cDNA clone (5'-primer) SEQ

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence was used as the representative sequence from a human clone which was used in homology searches to identify the clone. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full
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                                   GGTATCCGCTGCCTNCGTTATGAGATC
                                                                                                                                               TAGCTCAAACCATGAGATCAGAGCTCGGCAAACTCTCTNTGGACAAAGTCTTCCGGG
                                                                                                                                                                                                               TCATGGACCCTTACAAGGCAAGCTACGGTGTGGAGGACCCTGAGTATGCCGTCACCCAGC
ggtatccgctgcctccgttatnanatc
                                                              aacgggagtccctgaatgccagcattgtngatgccatccaaccaagctgctgantgctgg
                                                                                 AACGGGAGTCCCTGAATGCCAGCATTGTGGATGCCAT-CAACCAAGCTGCTGACTGCTGG
                                                                                                                                tagctcnaacaaccatganatnaganctcggcaaactctctctggacaaagtcttccggg
                                                                                                                                                                                             tcatggacccttacaacgcnagctacggtgtggaggaccctgagtatgccgtcacccagc
                                                                                                                                                                                                                                                               agtcggctgtgactctcgacaatgtaactctgcnaatcgatggagtcctttacctgcgca
                                                                                                                                                                                                                                                                              AGTCGGCTGTGACTCTCGACAATGTAACTCTGCAAATCGATGGAGTCCTTTACCTGCGCA
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Pred. No. 1.3e-136;
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CC full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of ct the 5602 nucleotide sequences defined in the specification, where the coligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprises a polynucleotide which comprises or the cc complementary strand of a polynucleotide which comprises a 5'-end cc complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the cc oligonucleotide comprises a 3'-end sequence, where the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primers are useful for synthesising polynucleotides, cc particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by ct the full-length cDNAs. The primers are also useful for the cDNAs easily without any specialised methods. AAH03166 to AAH13628 and CC AAB95893 represent human cDNA sequences; AAB92446 to cf the present oligonucleotides, all of which are used in the exemplification of the present invention.
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Best Local Similarity
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02-MAY-2000;
                                                                                                                                                                                                                                                                                   Sequence
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27-AUG-1999;
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TGGAGCGAATGGGCCGATTCCACCGGATCCTGGAGCCTGGTTTGAACATCCTCATCCCTG
                                         CCTCTGGATTGCCCCGAAACACCGTGGTACTGTTCGTGCCGCAGCAGGAGGCCTGGGTGG
                                                                                                                                                             ctggggcccttttgctgagggctctctactggcttctggccgcgctccgcgcgccct
                                                                                                                   CTGGGGCCCTTTTGCTGAGGGGCTCTCTACTGGCTTCTGGCCGCGCCTCCG-GCCGCGCCT 148
                                                                                                                                               cctctggattgccccgaaacaccgtggtactgttcgtgccgcagcaggaggcctgggtgg
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, Sugiyama
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; 2000JP-0241899.
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T, Wakamatsu
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97.0%;
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                                                                                                                                                                                                        Score 516.4;
Pred. No. 1.3e
0; Mismatches
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A, Nagai K,
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1.3e-136;
hes 14;
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Otsuki
                                                                                                                                                                                                                                                                                12 other;
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The present invention describes colon tumour associated proteins (I) and the polynucleotides (II) that encode them. (I) have cytostatic activity. (I) and (II) can be used in gene therapy and vaccine production. (I) and (II) may be used in the prevention, diagnosis and treatment of diseases

Claim

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English.

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15-FEB-2000;
06-MAR-2000;
19-MAY-2000;
29-JUN-2000;
28-AUG-2000;
                                                                                                                                                                                                                                                                                                                                    Human; immunotherapy; diagnosis; colon cancer; colon tumour; immunogenic; gene therapy; vaccine; colonic cancer; ss.
                                                                    prevention,
                                                                                                   WPI; 2001-441847/47
                                                                                                                                                                                                                                   30-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          associated with inappropriate colon tumour associated protein (TCAP) expression, such as colonic cancer. For example, (I) and (II) may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of TCAPs by expressing inactive proteins or to supplement the patients own production of them. Additionally, (II) may be used to produce the TCAP proteins, by inserting the nucleic acids into a host
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14 - MAR - 2000;
24 - MAR - 2000;
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15 - MAY - 2000;
09 - JUN - 2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to human breast cancer expressed polynucleotides (AAL07544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polynucleotides and encoded
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                         ggtgaaagagtctatgcagatgcatgtggaggcagaaccggcggaaacgggccgcaattc
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11-JAN-2000;
02-MAY-2000;
                                                      clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence was used as the representative sequence from a human clone which was used in homology searches to identify the clone.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; full length cDNA; cDNA synthesis; oligo-capping; ss
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AAK93925 standard; cDNA; 566 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to primers for synthesising full length cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 11; SEQ ID NO 2385; 1380pp + sequence listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HELI-) HELIX RES INST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Primers useful for synthesizing in genetic manipulation -
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tsu A, Sugiyama T, Nagai
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2000JP-0118774.
2000JP-0183765.
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K, Kojima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   full length cDNA clones and their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO: 2385.
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S, Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   761
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Query Match

Sequence

566

BP;

120 A;

152 C; 139

G; 155 T; 0 other;

Score 465.6;

В

22;

Length 566

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RESULT 1
ABL05449
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                                                                                                                                                                                                                               Drosophila melanogaster expressed polynucleotide SEQ ID NO 10829
                                                                                                                                                                                                                                                                                 ABL05449 standard; cDNA; 1153
                      New isolated nucleic acid genes from Drosophila and interactions .
                                                                                                                23-MAR-2000;
11-JUL-2000;
                                                                                                                                         23-MAR-2001; 2001WO-US09231
                                                                                                                                                        27-SEP-2001
                                                                                                                                                                                        Drosophila melanogaster.
                                                                                                                                                                                                       pharmaceutical; gene;
                                                                                                                                                                                                               Drosophila; developmental biology; cell signalling;
                                                                                                                                                                                                                                                26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 10829; 21pp + Sequence Listing; English.
                                                        WPI; 2001-656860/75.
P-PSDB; ABB61346.
                                                                                 Venter
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                                                                                 JC,
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                                                                                 Adams M,
                                                                                                                2000US-191637P
2000US-0614150
                                                                                                                                                                                                                                                (first entry)
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                               detection reagent for elucidating co
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ches 6;
                               nt for detecting cell signalling
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Query Match
Best Local Similarity
Matches 578; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
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TCCAACACTATCCTACTGCCCTCCAACCCTGGCGATGTCACCAGGCATGGTGGCTCAGGCC
                                                                                                                                                                                                                                                                                                                                                                                                    TCGGCCATCAATGTGGCAGAAGGGAAGGAAACAGGCCCCAGATCCTGGCCTCCGAAGCAGAA 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAGGTGGAGGCAGAGCGGCGGAGAACGGGCCACAGTTCTAGAGGTCTGAGGGGACCCCGAGAG
                                                                                                    GCAGCTTCACTGACTGTGGCCGAGCAGTATGTCAGCGCGCTTCTCCAAACTGGCCAAGGAC
                                                                                                                                                                                                    GCTAAAGCTGAAGCTATTCGAATCCTGGCTGCAGCTCTGACACAACATAATGGAGATGCA
                                                                                                                                                                                                                                                                                                       AAGGCTGAACAGATAAATCAGGCAGCAGGAGAGGCCAGTGCAGTTCTGGCGAAGGCCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          caagtggaggccgagcgaaagcgagccgctattctcgaatcggagggtgttcgcgag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGAATGCCAGCATTGTGGATGCCATCAACCAAGCTGCTGACTGCTGGGGTATCCGCTGC 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCATGAGATCAGAGCTCGGCAAACTCTCTNTGGACAAAGTCTTCCGGGAACGGGAGTCC 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACTCTCGACAATGTAACTCTGCAAAATCGATGGAGTCCTTTACCTGCGCATCATGGACCCT 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           atcaaatacgtccagagcctgaaggaaattgccatagatgtgcccaaacagagcgctatt 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATCCGATATGTGCAGAGTCTCAAGGAAATTGTCATCAACGTGCCTGAGCAGTCGGCTGTG 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGCCGATTCCACCGGATCCTGGAGCCTGGTTTGAACATCCTCATCCTCTGTGTTAGACCGG
                                                                        gctgcttcgctcacgctggccgagcagtacattggagccttcaagaagctggccaagacg
                                                                                                                                                                        cggcaggagcacatcaataaggccagcggagaggcggctgccattatagccgtggcggat 795
                                                                                                                                                                                                                                                                                                                                                                       gccgaaatcaacatagccgagggcaagcggaagtctaggattctagcctccgaggcggag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ctcaacgtcagcatcgtcgactcgatcaacaaggccagcgaggcgtggggcatcgcctgt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acgatgagatcggagctgggcaagatgtccatggacaaggtcttccgcgamagggagtcc
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Pred. No. 3.2e-105;
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Db 916 aataacaccatgatcttgccctcgaatcccggggatgttaatggcttcgtggcccaggcc 975

Qy 1000 ATGGGTGTATATGGAGCCCTCACCAA 1025
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Db 976 ctggcggtgtacaaccacgtttccaa 1001

Search completed: September 22, 2002, 15:26:24 Job time: 4289 sec

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1: /cgn2_6/ptodata/1,
2: /cgn2_6/ptodata/1,
3: /cgn2_6/ptodata/1,
4: /cgn2_6/ptodata/1,
5: /cgn2_6/ptodata/1,
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Maximum Match 100%
Listing first 45 summaries
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/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/BCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
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                US-08-464-954A-1
US-08-221-817-12
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PCT-US94-10487-10
US-08-221-817-10
PCT-US94-10487-10
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PCT-US94-10487-22
US-08-949-386-23
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US-08-232-463-14
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Compugen Ltd
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:

2.0

MEDIUM TYPE:

Diskette

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US-08-781-562-2

IMMEDIATE SOURCE:

TOPOLOGY:

linear

single

LIBRARY: Consensus CLONE: Consensus

INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 1188 base pairs

TELEX:

TYPE: nucleic acid STRANDEDNESS: sing

ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36, REFERENCE/DOCKET NUMBER:

36,749

PF-0181 US

TELEPHONE: 415-855-0555

TELEFAX: 415-845-4166

FILING DATE: Herewith CLASSIFICATION: 530 PRIOR APPLICATION DATA: APPLICATION NUMBER:

APPLICATION NUMBER:

Herewith

US/08/781,562

FILING DATE:

Query Match Best Local Similarity

99.6%; 100.0%;

Score 1183; Pred. No. 0;

DB 1;

Length 1188;

RESULT US-08- Sequ Pate Pate AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA		000
RESULT 1 US-08-781-562 Sequence 2, Patent NO. PAPLICAN APPLICAN APPLICAN TITLE OF NUMBER O CORRESPO ADDRES STREET CITY: STATE: COUNTR ZIP: COMPUTER		4444443337088 44444444444444444444444444444444444
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Application F5763589 FFORMATION: FFORMATION: FI Hillman, TI GOli, Sur TI SEQUENCES: F SEQUENCES ADDRES NDENCE ADDRES NDENCE ADDRES SEE: Incyte SEE: Incyte Palo Alto CA OCA OCA READABLE FOR		N N N N N N N N N N N N N M M M M M M M
Lication US/08:589 LATION: Hillman, Jenni. Goli, Surya K. Goli, Surya K. TOUENTION: NOVEL TOUENCES: TOUENES: Incyte Pharm 1174 Porter Driv O Alto USA UDSA		1100 1100 13842 38678 38506 2018 2017 2277 2277 2277 8255 8252 8252 8257 8257
US/087815  Jennifer ya K. NOVEL HUM 7 7 S: S: Pharmaceu r Drive		3 3 2 3 3 1 1 1 2 1 1 2 3 3 3 4 4 3 3 2 1
cation US/08781562  JON: Jennifer L. Li, Surya K. TION: NOVEL HUMAN MEMBRANE PROTEIN ENCES: ENCES: ADDRESS: Incyte Pharmaceuticals, Inc. A Porter Drive Alto A A	ALIGNMENTS	US-07-949-516A-1 US-08-814-459-1 US-09-122-525-1 US-09-105-537-30 US-09-105-537-5 US-09-105-537-5 US-09-141-000-2 US-08-676-974-2 US-08-676-974-2 US-08-676-974-2 US-08-676-974-2 US-08-08-676-974-2 US-08-08-115 US-08-93-703-15 US-08-942-008-1 US-08-735-041A-3 US-09-190-489A-3
		Sequence 1, Appli Sequence 1, Appli Sequence 30, Appli Sequence 5, Appli Sequence 5, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli

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                                             TCCAACCCTGGCGATGTCACCAGCATGGTGGCTCAGGCCATGGGTGTATATGGAGCCCTC
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; TOPOLOGY: Linear
; IMMEDIATE SOURCE:
; CLONE: pTZqpt-F1s
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Matches 8
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TELEX: 899149
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
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ZIP: 22313-0299

ZIP: 22313-0299

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
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                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
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APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1081
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE:
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CITY: Alexandria
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
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AGATCCTGGCCTCCGAAGCAGAAAAGGCTGAACAGATAAATCAGGCAGCAGGAGAGAGCCCA
                                                                                                                                                            Similarity
8; Conserv
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                                                                                                                                                          4.1%; Score 48.8; DB 1; llarity 2.6%; Pred. No. 0.00051; Conservative 184; Mismatches 116;
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Best Local Similarity
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Patent No. 5691460
                                                                                                                                                                                 Matches 153;
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APPLICANT: Duvic, Madeleine
APPLICANT: Schroeder, Wanda T
                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 2488 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/320-7200
TELEFAX: 512/474-7577
                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Mayfield, Denise L.
REGISTRATION NUMBER: 33,7
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Epidermal Surface Antigen and Uses TITLE OF INVENTION: Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1062 CAAGCTCC 1055
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GGATGCCATCAACCAAGCTGCTGACTGCTGGGGGTATCCGCTGCCTNCGTTATGAGATCAA 596
                                                                                                                                             TGTGGAGGACCCTGAGTATGCCGTCACCCAGCTAGCTCAAACAACCATGAGATCAGAGCT 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGTTCTCC
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                                               CGGGACCCTGACAGTGGAGCAGATTTATCAGGACCGGGACCAGTTTGCCAAGCTGGTGCG
                                                                               CGGCAAACTCTCTNTGGACAAAGTCTTCCGGGAACGGGAGTCCCTGAATGCCAGCATTGT 536
                                                                                                               TGTGCAGGACATCAAAAACGTCGTCCTGCAGACCCTGGAGGGACATCTGCGCTCCATCCT 323
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                                                                                                                                                                               0;
                                                                                                                                                                                              Score 39.6; DB Pred. No. 0.12;
                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Version
                                                                                                                                                                                                            DB 1;
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                                                                                                                                                                                                          Length. 2488;
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; ANTI-SENSE:
US-08-464-954A-1
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US-08-464-954A-1
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                                                                                                                       Matches
                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                            TELEFAX: (609) 779-8488 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/0
FILING DATE: June 11, 19
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: JE
TELECOMMUNICATION INFORMATION:
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: DISKETT
                                                   1317 CCGACTACTGGGGCCTTGGCTGCCTCATCTATGAGATGATCGAGGGCCAGTCGCCGTTCC 1376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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617 GGGTGAAAGAGTCTATGCAGATGCAGGTGGAGGCAGAGCGGGGAAACGGGCCACAG 673
                                                                                    557 CTGACTGCTGGGGTATCCGCTGCCTNCGTTATGAGATCAAGGATATCCATGTGCCACCCC 616
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CITY: C
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STREET: Woo
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                                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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                                                                                                                                                                                                                                                                                         LENGTH:
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                                                                                                                     Conservative
                                                                                                                                                                                                                          LINEAR
NO
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                                                                                                                                                                                                                                                                                                                                                            (609)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JEFFREY L.; GOMEZ, JORGE; KUNAPULI
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                                                                                                                    Score 39.2; DB 4;
Pred. No. 0.16;
0; Mismatches 49;
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                                                                                                                       49;
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1377 GCGGCCGTAAGGAGAAGGTGAAGCCGGAGGAGGTGGACCGCCGGGTCCTGGAGACGG 1433

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US-08-221-817-12
US-08-454-439-12

Sequence 12, Application US/08454439

: Patent No. 5591618

: GENERAL INFORMATION:
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; LOCATION:
US-08-221-817-12
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TELEPHONE: (312) 474-6300
TELEPAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 2204 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Sequence 12, App
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Best Local Similarity
Matches 63; Conserv
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/123,932
FILING DATE: 17 SEP 1993
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5532151and, Greta E.
REGISTRATION NUMBER: 35,302
REGISTRATION NUMBER: 35,302
REGISTRATION NUMBER: 31981
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hoekstra, Merle F.
TITLE OF INVENTION: A No. 5532151el G Protein-Coupled Receptor
TITLE OF INVENTION: Kinase GRK6
                                                                                                                                                                                                            1127
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                                                                                                                                  1187
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                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: CDNA
                                                                                                                                                                     617 GGGTGAAAGAGTCTATGCAGATGCAGGTGGAGGCAGAGCGGCGG 660
                                                                                                                                                                                                                                 557 CTGACTGCTGGGGTATCCGCTGCCTNCGTTATGAGATCAAGGATATCCATGTGCCACCCC 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
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                                                                                                                                                                                                          CTGACTGGTGGGCGCTCGCCTGCCTGTACGAGATGATCGCAGGCCAGTCGCCCTTCC 1186
                                                                                                                                  AGCAGAGGAAGAAGAAGATCAAGCGGGAGGAGGTGGAGCGGCTG 1230
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: Illinois
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chantry, David
                                                                                                                                                                                                                                                                                    Conservative
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; Sequence 12, Application PC/TUS9410487
; GENERAL INFORMATION:
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Best Local Similarity
Matches 63; Conserv
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APPLICATION NUMBER: US 08,
FILING DATE: 31-MAR-1994
APPLICATION UMBER: 08/123
FILING DATE: 17 SEP 1993
CCLASSIFICATION: 435
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5591618and, Greta
NAME: No. 5591618and, Greta
NAME: No. 5591618and, Greta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 30-MAY-19
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                       1187
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                                                                                                                                                                                                                                                                        1127 CTGACTGGTGGGCGCTCGGCTGCCTCCTGTACGAGATGATCGCAGGCCAGTCGCCCTTCC 1186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 2204 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: cDNA
                                            APPLICANT: ICOS COR
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
              CORRESPONDENCE ADDRESS:
                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                         617 GGGTGAAAGAGTCTATGCAGATGCAGGTGGAGGCAGAGCGGCGG 660
                                                                                                                                                                                                                                                                                           557 CTGACTGCTGGGGTATCCGCTGCCTNCGTTATGAGATCAAGGATATCCATGTGCCACCCC 616
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION:
                                                                                                                                                                                                     60606
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6300 Sears Tower, 233 South Wacker Drive
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Hoekstra, Merle F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (312) 474-0448
                                                                                  ICOS Corporation
                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Marshall, O'Toole, Gerstein, Murray
Marshall,
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                            A Novel G Protein-Coupled Receptor
Kinase GRK6
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O'Toole, Gerstein, Murray &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Greta E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31981
                                                                                                                                                                                                                                                                                                                                              Score 39; DB Pred. No. 0.17
                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
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ADDRESSEE: Borun STREET: 6300 Sea: CITY: Chicago STATE: Illinois

Borun

6300 Sears Tower, 233 South Wacker Drive

COUNTRY:

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RESULT 8
US-08-221-817-10
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                                                                                                                                                                                                           Sequence 10
Patent No.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                            GENERAL INFORMATION:
                                                              APPLICANT: Chantry, David
APPLICANT: Gray, Patrick W.
APPLICANT: HoekStra, Merle F.
TITLE OF INVENTION: A No. 5532151el G Protein-Coupled Receptor
TITLE OF INVENTION: Kinase GRK6
NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                    1187 AGCAGAGGAAGAAGAAGATCAAGCGGGAGGAGGTGGAGCGGCTG 1230
                                                                                                                                                                                                                                                                                                                                                                                      1127 CTGACTGGTGGGCGCTCGGCTGCCTCCTGTACGAGATGATCGCAGGCCAGTCGCCCTTCC 1186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                     617 GGGTGAAAGAGTCTATGCAGATGCAGGTGGAGGCAGAGCGGCGG
                                                                                                                                                                                                                                                                                                                                                                                                           557 CTGACTGCGGGGTATCCGCTGCCTNCGTTATGAGATCAAGGATATCCATGTGCCACCCC 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/2 FILING DATE: 31 MAR 1994 CLASSIFICATION:
            STREET:
                               ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/1 FILING DATE: 17 SEP 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
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                                                                                                                                                                                                              10, Application US/08221817
5. 5532151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                63;
Chicago
            6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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US-08-454-439-10
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; LOCATION:
US-08-221-817-10
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10, Approx. 5591618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRILLING DATE:
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/123
APPLICATION NUMBER: 1993
                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATE: 17 SET T.

FILING DATE: 17 SET T.

ATTORNEY AGENT INFORMATION:

ATTORNEY NO. 553215land, Greta

NAME: NO. 553215land, Greta

NAME: NO. 353215land, Greta

NAME: NO. 353215land, Greta

NAME: NO. 353215land, Greta
                                                                                                                   STREET: Chicago
CITY: Chicago
TMATE: Illinois
                                                                                                                                                                                                                                                                                APPLICANT: Chantry, David
APPLICANT: Gray, Patrick W.
APPLICANT: Hoekstra, Merie F.
TITLE OF INVENTION: A No. 5591618el G Protein-Coupled Receptor
TITLE OF INVENTION: Kinase GRK6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1124 CTGACTGGTGGGCGCTCGGCTGCCTCCTGTACGAGATGATCGCAGGCCAGTCGCCCTTCC 1183
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LENGTH: 2206 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELERAX: (312) 474-0448
TELERAX: 25-3856
                                                         MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1184 AGCAGAGGAAGAAGATCAAGCGGGAGGAGGTGGAGCGGCTG 1227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          557 CTGACTGCTGGGGTATCCGCTGCCTNCGTTATGAGATCAAGGATATCCATGTGCCACCCC 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              617 GGGTGAAAGAGTCTATGCAGATGCAGGTGGAGGCAGAGCGGCGG 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                 ADDRESSEE:
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                                                                                                     60606
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                                                                                                                                                                               6300 Sears Tower, 233 South Wacker Drive
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                                                                                                                                                                                                                    Marshall, O'Toole, Gerstein, Murray
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    Version #1.25
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Gaps

0;

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
US. 08/221,817

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US

FILING DATE:

30-MAY-1995

US/08/454,439

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APPLICATION NUMBER: 08/123,932
APPLICATION NUMBER: 08/123,932
FILING DATE: 17 SEP 1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5591618and, Greta E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (312) 474-044
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1124 CTGACTGGTGGCCTCCGCTGCCTCCTGTACGAGATGATCGCCAGGCCAGTCGCCCTTCC 1183
                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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LENGTH: 2206 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (312) 474-6300
              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/2
FILING DATE: 31 MAR 1994
                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: A Novel G Protein-Coupled Receptor TITLE OF INVENTION: Kinase GRK6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     617 GGGTGAAAGAGTCTATGCAGATGCAGGTGGAGGCAGAGCGGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  557 CTGACTGCTGGGGTATCCGCTGCCTNCGTTATGAGATCAAGGATATCCATGTGCCACCCC 616
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (312) 474-0448
                                                                                                                                                                                                                                                                                               STREET: 6300 Sea
CITY: Chicago
STATE: Illinois
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CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 35, REFERENCE/DOCKET NUMBER:
                                                                                                 FILING DATE:
                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                         ZIP: - 60606
                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
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63; Conservative
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                                                                                                                                                                                                                                                                                                                                         6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ICOS Corporation
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31..1926
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                                                                                                                                                                                                                                                                                                                                                                Borun
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                                                                                                                  PCT/US94/10487
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RESULT 11
US-08-149-097D-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 23, Application US/08149097D
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Best Local 9
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1124 CTGACTGGTGGGCGCTCGGCTGCCTCTGTACGAGATGATCGCAGGCCAGTCGCCCTTCC 1183
                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1184 AGCAGAGGAAGAAGAAGATCAAGCGGGAGGAGGTGGAGCGGCTG 1227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION: NAME: Noland, Greta E.
             APPLICATION NUMBER: 08/11 FILING DATE: 11-AUG-1993 PRIOR APPLICATION DATA:
                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                           SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: (312) 474-6300
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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CLASSIFICATION:
                                                                                            APPLICATION NUMBER: FILING DATE: 05-NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Noland, Greta E. REGISTRATION NUMBER: 35, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                            CITY: San Diego
                                                                                                                                                                                                                                                                                         STREET:
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 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2206 base pairs
                                                                                                                                                                                                                                                                                        E: Brown, Martin, Haller & McClain
1660 Union Street
                                                                                                                                                                                                                                                                                                                                                                                                                        Williams, Mark
Feldman, Daniel
                                                                                                                                                                                                                                            USA
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                                                                                                                                                                                                                                                                                                                                                                                                         McCue, Ann
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                                                                                              05-NOV-1993
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                                                                                                                                                                                                                                                                                                                                                           METHODS
                                                08/105,536
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                                                                                                             US/08/149,097D
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WO PCT/US92/06903
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Pred. No. 0.17;
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                                                                                                                                               Version #1
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PRIOR APPLICATION DATA:

13-JUL-1992

US 07/868,354

US 07/914,231

FILING DATE: 14-AUG-PRIOR APPLICATION DATA:

14-AUG-1992

APPLICATION NUMBER:

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; NAME/KEY: CDS;; LOCATION: 240..7037; LOCATION: 240..7037; OTHER INFORMATION: /product= "Alphala-2 subunit of; OTHER INFORMATION: human calcium channel" US-08-149-097D-23
               RESULT 12
US-08-949-386-23
: Sequence 23, Application US/08949386
; Patent No. 6090623
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Best Local Similarity
Matches 111; Conserv
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                       2393
                                                                                                                      2513 CATGTCTATAGCTGTGAAAGAGCAACAGAAGAATCAAAAGCCCAGCCAAGTCC
                                                                                                                                                                                                                                                                                                                                         2333 CTTTGGGAACTACACCCTCCTGAATGTGTTCTTGGCCATCGCTGTGGACAATCTGGCCAA 2392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 04-APR-1988 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: WO PILING DATE: 04-APR-1989 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 20-FEB-1990 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                           624
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                                                                                                                                                          744 GGCCTCCGAAGCAGAAAAGGCTGAACAGATAAATCAGGCAGCAGGAGAGGCC
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                                                                                                                                                                                            GAAACTTGCCCTACAGAAAGCCAAGGAGGTGGCAGAAGTGAGTCCTCTGTCCGCGGCCAA 2512
                                                                                                                                                                                                                                TGAGGGGACCCGAGAGTCGGCCATCAATGTGGCAGAAGGGAAGAAACAGGCCCCAGATCCT 743
                                                                                                                                                                                                                                                                   CGCCCAGGAGCTCACCAAGGTGGAGGCGACGACGAGCAAGAAGAAGAAGCAGCGAACCA 2452
                                                                                                                                                                                                                                                                                                     AGAGTCTATGCAGATGCAGGTGGAGGCAGAGCGGCGGAAACGGGCCACAGTTCTAGAGTC 683
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RATION NUMBER: 33,779
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47.8%;
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0.31;
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2393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 11-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 11-AUG-1994
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TITLE OF INVENTION: HUMAN CA
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 38
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APPLICANT:
                          744 GGCCTCCGAAGCAGAAAAGGCTGAACAGATAAATCAGGCAGCAGGAGAGGCC 795
                                                                                          624 AGAGTCTATGCAGATGCAGGTGGAGGCAGAGCGGCGGAAAACGGGCCACAGTTCTAGAGTC
                                                                                                                                                                                                            564 CTGGGGTATCCGCTGCTTATGAGATCAAGGATATCCATGTGCCACCCCGGGTGAA 623
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STREET: 16
CITY: San
                                                                                                                                                                                                                                                         Local Similarity 47.8
es 111; Conservative
                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
LOCATION: 237..7037
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/:
FILING DATE: 5-NOV-1993
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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                                                                                                                          CGCCCAGGAGCTCACCAAGGTGGAGGCGACGACGAGCAAGAAGAAGAAGCAGCGAACCA 2452
                                                                                                                                                                                         CTTTGGGAACTACACCCTCCTGAATGTGTTCTTGGCCATCGCTGTGGACAATCTGGCCAA
                                                            GAAACTTGCCCTACAGAAAGCCAAGGAGGTGGCAGAAGTGAGTCCTCTGTCCGCGGCCAA 2512
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EDNESS: double
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Ellis, Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Williams, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                     DNA (genomic)
                                                                                                                                                                                                                                                                      3.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HUMAN CALCIUM CHANNEL COMPOSITIONS AND
                                                                                                                                                                                                                                                                                                                                                   /standard_name= "Alpha-1A-2"
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                                                                                                                                                                                                                                                                        Score 39; DB 3 Pred. No. 0.31;
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                                                                                                                                                                                                                                                       Mismatches
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2564
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US-08-450-562-23
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                            FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0'
FILING DATE: 5-NOV-19
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/404
FILING DATE: 13-MAR-1995
APPLICATION NUMBER: 08/33(
FILING DATE: 7-NOV-1994
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Feldman, Danies APPLICANT: Feldman, Robert TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND TITLE OF INVENTION: METHODS
                                                                                                                                   FILING DATE: 10-APR-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/914,231
FILING DATE: 13-JULY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/2 FILING DATE: 11-AUG-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 23-SEPTPRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/314,083
FILING DATE: 28-SEPT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                   PRIOR APPLICATION DATA:
                                                                                   FILING DATE: 14-AUG-
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: 07/6
                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/10 FILING DATE: 11-AUG-1993
                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08/1:
FILING DATE: 07-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/31
                                                   APPLICATION NUMBER: 07/7 FILING DATE: 15-AUG-1991
                                                                                                     APPLICATION NUMBER: PCT/
FILING DATE: 14-AUG-1992
                                                                                                                                                                        APPLICATION NUMBER:
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CITY: San Diego
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Ellis, Steven
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; OTHER INFORMATION:
US-08-450-562-23
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US-08-984-709A-23
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                                                                                                                                                                                                                                                                    Sequence 23, Applicat: Patent No. 6320032 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match Best Local Similarity Matches 111; Conserv
                                                                                                                                                                       APPLICANT: Williams, Mark E.
APPLICANT: Stauderman, Kenneth A.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS
TITLE OF INVENTION: METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 07/482,384
FILING DATE: 02-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/482,384
                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                         2453 GAAACTTGCCCTACAGAAAGCCAAGGAGGTGGCAGAAGTGAGTCCTCTGTCCGCGGCCAA 2512
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                           744 GGCCTCCGAAGCAGAAAAGGCTGAACAGATAAATCAGGCAGCAGGAGAGGCC 795
                                       COUNTRY:
                                                       CITY: La Jolla
STATE: California
                                                                                             STREET:
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                                                                                             ADDRESSEE: Heller Ehrman White & McAuliffe STREET: 4250 Executive Square, Suite 700
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LOCATION: 237..7037
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                       92037
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NO: 23:
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47.8%;
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Pred. No. 0.31;
0; Mismatches
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Best Local Similarity
Matches 111; Conserv
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                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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LENGTH: 7791 base pairs
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REFERENCE/DOCKET NUMBER: 24735-9815 (formerly 6362-9815)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 450-8400
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                                                                                                                                                                        APPLICANT: Brenner, Robert TITLE OF INVENTION: HUMAN CTITLE OF INVENTION: METHODS
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                       2393 CGCCCAGGAGCTCACCAAGGTGGAGGCGACGAGCAAGAAGAAGAAGAAGCAGCGAACCA 2452
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                                                                                                                                                          NUMBER OF SEQUENCES:
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LOCATION: 237..703
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Seidman, Stephanie L. REGISTRATION NUMBER: 33,779
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COMPUTER: I
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STRANDEDNESS: double
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                                                                                     CITY: San Diego
                                                                                                     STREET:
                                       ZIP:
                                                 COUNTRY:
                                                                        STATE:
                                                                                                                       ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGCCTCCGAAGCAGAAAAGGCTGAACAGATAAATCAGGCAGCAGGAGAGGCC 795
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                                      92101-2926
                                                                                                                                                                                                                                                                                                                                     5874236
                                                                      California
                                                                                                                                                                                                                                                                                                                                                   Application US/08149097D
                                                                                                       1660 Union Street
                                                      USA
                                                                                                                                                                                                                             McCue, Ann
                                                                                                                                                                                                                                          Williams, Mark
Feldman, Daniel
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Ellis, Steven
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                                                                                                                      Brown, Martin, Haller & McClain
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02-DEC-1997
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                                                                                                                                                                          HUMAN CALCIUM CHANNEL COMPOSITIONS AND METHODS
                                                                                                                                                          40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /standard_name= "Alpha-1A-2"
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Pred. No.
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QΥ
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                                                                                                                                                                                                             Matches 111;
                                                                                                                                                                                                                               Query Match 3.3%;
Best Local Similarity 47.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (619) 238-0062
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 63
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Rel-
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 04-APR-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 20-FEB-1990 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 11-AUG-
PRIOR APPLICATION DATA:
                                                         2393 CGCCCAGGAGCTCACCAAGGTGGAGGCGGACGAGCAAGAGGAAGAAGAAGCAGCGAACCA 2452
                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                         564 CTGGGGTATCCGCTGCCTNCGTTATGAGATCAAGGATATCCATGTGCCACCCCGGGTGAA 623
684 TGAGGGGACCCGAGAGTCGGCCATCATGTGGCAGAAGGGAAGAAAACAGGCCCAGATCCT 743
                                                                                             624 AGAGTCTATGCAGATGCAGGTGGAGGCAGAGCCGGCGAAACGGGCCACAGTTCTAGAGTC 683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: WO POSTILLING DATE: 04-APR-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 0' FILING DATE: 30-NOV-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US US PITTING DATE: 10-APR-1992
                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 07/745,206 FILING DATE: 15-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 14-AUG-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: 240..7769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                 CTTTGGGAACTACACCCTCCTGAATGTGTTCTTGGCCATCGCTGTGGACAATCTGGCCAA 2392
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EDNESS: single
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                                                                                                                                                                                                             Conservative
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11-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                           DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stephanie L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 238-0999
                                                                                                                                                                                                                                                                                                                             /product= "AlphalA-1 subunit of
human calcium channel"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US 07/176,899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US 07/603,751,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US 07/482,384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US 07/620,250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO PCT/US89/01408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US 07/868,354
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                                                                                                                                                                                                             0;
                                                                                                                                                                                                                               Score 39; DB 2; Length 7808; Pred. No. 0.31;
                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                             121; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #1.25
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0;

Search completed: September 22, 2002, 15:22:50 Job time: 6995 sec

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Run
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Searched:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OM nucleic - nucleic search, using sw model
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                                                                                                                                                                                     Pending_Patents_NA_Main:*
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Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-898-216-2
1188
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                                         cgn2_6/ptodata/1/pna/US081_COMB.seq:*
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c/gn2_6/ptodata/1/pn
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Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGCTTCTGGGAGCNACCGCT..........GGAAGCAGATTTTCCTGATT 1188
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/cgn2_6/ptodata/1/pna/US6003_COMB.seq:*
/cgn2_6/ptodata/1/pna/US6004_COMB.seq:*
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46 //cgn2_6/ptodata/1/pna/US6007_COMB.seq: *
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75 //cgn2_6/ptodata/1/pna/US6035_COMB.seq: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.

Query Score Match Length DB

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Description

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27 28 29 30 31	10 98 11 11 11 11 11 11 11 11 11 11 11 11 11	7654321
1072 1072 1072 1072 1067.6 1067.6	1155 1155 1155 1155 1155 1155 1155 115	1166 1160 1160 1160 1160
90.2 90.2 89.9	9722 9722 9722 9722 9722 9722 963	
1308 1308 1308 1501 1501	1384 13884 13884 13884 13884 13884 13884 13337 13337 14166 14166 1429 1429 1429 1429 1429 1429 1429 1429	1322 1322 1398 1398 1398 1398
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US-09-340-623-13379 US-09-898-888-13379 US-09-898-888A-13379 US-09-298-733-35 US-09-298-733A-35	US-09-338-467-941 US-09-644-869-8024 US-09-652-109-7925 US-09-652-127-7358 US-09-652-117-7358 US-09-652-913-809 US-09-652-914-7997 US-09-652-914-7997 US-09-808-384-941 PCT-US98-1215-45 PCT-US98-1215-45 US-09-209-4628-45 PCT-US01-04098A-24 US-09-598-075A-24 US-09-598-075A-249 US-60-1172-373-10483 PCT-US01-04942A-34 US-09-596-1193A-37 US-60-124-285-3468 US-09-205-070-13379	PCT-US98-12125-102 US-09-209-462B-106 PCT-US01-03800A-1001 PCT-US01-04098A-2212 US-09-471-275-865 US-09-496-914A-8410 US-09-496-914A-8410
Sequence 13379, A Sequence 13379, A Sequence 13379, A Sequence 35, Appl Sequence 35, Appl	Sequence 941, App Sequence 7309, Ap Sequence 7358, Ap Sequence 7419, Ap Sequence 7419, Ap Sequence 797, Ap Sequence 241, App Sequence 45, App Sequence 45, App Sequence 244, App Sequence 249, App Sequence 31, App Sequence 31, App Sequence 31, App Sequence 34, App Sequence 3468, Ap Sequence 3468, Ap Sequence 3468, Ap Sequence 3468, Ap	102, A 106, 1001, 2212, 865, 8410,

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PCT-US98-12125-102
Sequence 102, Application PC/TUS9812125
GENERAL INFORMATION:
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                                                                                                                                                                                          ; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
PCT-US98-12125-102
                                                                                                                                                                                                                                               NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PZ008Complete
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8439
INFORMATION FOR SEO ID NO: 102:
SEQUENCE CHARACTERISTICS:
LENGTH: 1322 base pairs
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Best Local S
Matches 1177
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STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READBALE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4
COMPUTER: HP Vectta 486/33
OPERATING SYSTEM: MSDOS Version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US98/12125
FILING DATE: Jan 01, 1900
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UMBER:
FILING DATE: TORNATION:
APPLICATION DATA:
APPLI
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TITLE OF INVENTION: 86 Human Secreted Proteins
NUMBER OF SEQUENCES: 318
CORRESPONDENCE ADDRESS:
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nes 1177; Conserv
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AATGCTGGCGCGCGCGCGCCC-GNGGCACTGGGGGCCCCTTTTGCTGAGGGGCCTCTCTACTGG
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10 US-09-818-134-349
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17 US-10-1185-213-1569
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PRIOR APPLICATION NUMBER: 60/04
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APPLICANT: R
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                                                      NUMBER OF SEQ ID NOS:
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OR APPLICATION NUMBER: 60/05
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OR FILING DATE: 1997-06-13
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OR APPLICATION NUMBER: 60/050,901
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APPLICANT: Hyseq, Inc.

APPLICANT: Hyseq, Inc.

APPLICANT: Tang, Y, Tom et al

TITLE OF INVENTION: NOVel Nucleic Acids and Pol

FILE REFERENCE: 21272-030

CURRENT APPLICATION NUMBER: PCT/US01/03800A

CURRENT FILING DATE: 2001-02-05

PRIOR APPLICATION NUMBER: 09/560,875

PRIOR APPLICATION NUMBER: 09/496,914

PRIOR FILING DATE: 2000-04-27

PRIOR FILING DATE: 2000-02-03

NUMBER OF SEQ ID NOS: 2700

SOFTWARE: Custom

SEQ ID NO 1001

LENGTH: 1398

TYPE: DNA

ORGANISM: Homo Sapiens

PCT-US01-03800A-1001
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Sequence 1001, Application
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RESULT 4

PCT-USO1-04098A-2212/c

PCT-USO1-04098A-2212/c

; Sequence 2212, Application PC/TUS0104098A
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 21277-029
; CURRENT APPLICATION NUMBER: PCT/US01/04098A
; CURRENT FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: Not Yet Assigned

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Best Local Similarity
Matches 1182; Conser
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OR APPLICATION NUMBER: 09/728,422
OR FILING DATE: 2000-11-30
OR APPLICATION NUMBER: 09/693,325
OR FILING DATE: 2000-10-20
OR FILING DATE: 2000-09-15
OR APPLICATION NUMBER: 09/654,936
OR APPLICATION NUMBER: 09/654,936
OR APPLICATION NUMBER: 09/620,325
OR FILING DATE: 2000-09-01
OR APPLICATION NUMBER: 09/580,325
OR FILING DATE: 2000-07-19
OR APPLICATION NUMBER: 09/598,075
OR APPLICATION NUMBER: 09/598,075
OR APPLICATION NUMBER: 09/590,075
OR APPLICATION NUMBER: 09/590,075
OR APPLICATION NUMBER: 09/590,075
OR APPLICATION NUMBER: 09/590,075
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APPLICATION NUMBER: 09/496,914
OFFICE DATE: 2000-02-03
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TATCCATGTGCCACCCCGGGTGAAAGAGTCTATGCAGATGCAGGTGGAGGCAGAGCGGCG
                                                                                             GTTCGTGCCGCAGCAGGAGGCCTGGGTGGATGGACGAATGGGCCGATTCCACCGGATCCT
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APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVel
TITLE OF INVENTION: NOVel
TITLE OF INVENTION: From V
FILE REFERENCE: 782
CURRENT FILING DATE: 1999EARLIER APPLICATION NUMBER
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ER FILING DATE: 1999-01-22
ER APPLICATION NUMBER: US 09/240,3:
ER FILING DATE: 1999-01-9
ER APPLICATION NUMBER: US 09/277,2:
ER FILING DATE: 1999-03-25
ER APPLICATION NUMBER: US 09/271,4:
ER FILING DATE: 1999-03-18
ER FILING DATE: 1999-03-18
ER APPLICATION NUMBER: US 09/293,9:
ER APPLICATION NUMBER: US 09/274,8:
ER APPLICATION NUMBER: US 09/274,8:
ER FILING DATE: 1999-03-23
ER FILING DATE: 1999-03-23
ER FILING DATE: 1999-03-23 ER APPLICATION NUMBER: US 60
ER FILING DATE: 1999-03-26
ER FILING DATE: 1999-05-07
ER FILING DATE: 1999-05-07
ER APPLICATION NUMBER: US 09
ER FILING DATE: 1999-09-21
ER FILING DATE: 1999-09-21
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ER FILING DATE: 1999-09-21 APPLICATION NUMBER: US/09/471.
FILING DATE: 1999-12-23
APPLICATION NUMBER: US 09/235.
FILING DATE: 1999-01-20 APPLICATION NUMBER: US (FILING DATE: 1999-03-19 Novel Various Libraries Contigs 09/399 09/306 60/126, 60/125, 09/274,861 09/271,490 09/234,611 09/404 Obtained

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NUMBER OF SEQ ID NOS: 10451

SOFTWARE: pt_CT_genes Version 1.0

SEQ ID NO 865

LENGTH: 1398

TYPE: DNA

ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1296)...(264)
OTHER INFORMATION: SINIlar to g12984585 in the genepept database release 1
OTHER INFORMATION: Run with FASTXY 3.3t00, default parameters
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Best Local Similarity 99.4
Matches 1182; Conservative
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                                                       GAAACGGGCCACAGTTCTAGAGTCTGAGGGGACCCGAGAGTCGGCCATCAATGTGGCAGA
                                                                                               CAAACTCTCTNTGGACAAAGTCTTCCGGGAACGGGAGTCCCTGAATGCCAGCATTGTGGA
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                 AGGGAAGAACAGGCCCAGATCCTGGCCTCCGAAGCAGAAAAGGCTGAACAGATAAATCA
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GGCAGCAGGAGAGGCCAGTGCAGTTCTGGCGAAGGCCAAGGCTAAAGCTGAAGCTATTCG
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1.6e-278;
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APPLICANT: LILING Chenghus
APPLICANT: LILING Chenghus
APPLICANT: LILING Chenghus
TITLE OF INVENTION: Novel Contigs Obtained
TITLE OF INVENTION: NOVEL CONTIGEN
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GENERAL INFORMATION:
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APPLICANT:
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Tillinghast, i
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PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: US 60/125,453
PRIOR APPLICATION UNMBER: US 60/126,605
PRIOR FILING DATE: 1999-03-26
PRIOR PRIOR PRICATION NUMBER: US 60/126,605
PRIOR FILING DATE: 1999-03-26
PRIOR EILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: US 09/309,720
PRIOR APPLICATION NUMBER: US 09/399,720
PRIOR FILING DATE: 1999-09-21
PRIOR FILING DATE: 1999-09-21
PRIOR FILING DATE: 1999-09-21
PRIOR APPLICATION NUMBER: US 09/465,877
PRIOR APPLICATION NUMBER: US 09/465,877
PRIOR APPLICATION NUMBER: NOT YET ASSIGNED PRIOR APPLICATION NUMBER: NOT YET ASSIGNED PRIOR APPLICATION NUMBER: NOT YET ASSIGNED PRIOR FILING DATE: 1999-01-19
NUMBER OF SEQ ID NOS: 10410
SOFTWARR: PLCT_genes Version 1.02
SEQ ID NO 8410
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Best Local Similarity
Matches 1182; Conserv
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FEATURE:
NAME/KEY: misc_feature
LOCATION: (1296)...(254)
OTHER INFORMATION: similar to gi2984585 in the genepept database
OTHER INFORMATION: Run with FASTXY 3.3t00, default parameters
-09-496-914A-8410
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FILING DATE:
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GCAAATCGATGGAGTCCTTTACCTGCGCATCATGGACCCTTACAAGGCAAGCTACGGTGT
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                                                                                CAAACTCTCTNTGGACAAAGTCTTCCGGGAACGGGAGTCCCTGAATGCCAGCATTGTGGA
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                                                               CAAACTCTCTGGACAAAGTCTTCCGGGAACGGGAGTCCCTGAATGCCAGCATTGTGGA
                                                                                                                               GGAGGACCCTGAGTATGCCGTCACCCAGCTAGCTCAAACAACCATGAGATCAGAGCTCGG
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Pred. No. 2
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1296)...(264)
; OTHER INFORMATION: similar to gi2984585 in the genepept database
; OTHER INFORMATION: Run with FASTXY 3.3100, default parameters
US-09-560-875A-8410
                                                                                                                                                                                                                                                                                              RESULT 7
US-09-560-875A-8410/c
S-09-60-88410, Application US/09560875A
GENERAL INFORMATION:
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                                                                                                  SOFTWARE: pt_CT_genes Version 1.02
SEQ ID NO 8410
LENGTH: 1398
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APPLICANT:
APPLICANT:
APPLICANT:
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TITLE OF INVENTION: Novel Contigs Obtained
TITLE OF INVENTION: From Various Libraries
FILE REFERENCE: 787
                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/560,875A CURRENT FILING DATE: 2000-04-27
                                                                                                                                        Prior application data removed - NUMBER OF SEQ ID NOS: 10410
                                                                                                                                                                                                                                                                  APPLICANT: Tang, Yuanhua T.
APPLICANT: Tillinghast, John
                                                                                        LENGTH: 13
                                                                          ORGANISM: Homo sapiens
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Liu, Chenghua
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Query Match
Best Local Similarity

97.6%;

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                                                           CGAGCAGTATGTCAGCGCGTTCTCCAAACTGGCCAAGGACTCCAAQ
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APPLICANT: Gearing, David P.
APPLICANT: Holtzman, Douglas A.
APPLICANT: Holtzman, Douglas A.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES DEI
TITLE OF INVENTION: HUMAN PROSTATE STROMAL LII
FILE REFERENCE: MLN98-25p
CURRENT APPLICATION NUMBER: US/09/338,467
CURRENT FILING DATE: 1999-06-22
EARLIER APPLICATION NUMBER: 60/990,177
EARLIER APPLICATION NUMBER: 60/990,177
EARLIER FILING DATE: 1998-06-22
NUMBER OF SEQ ID NOS: 1022
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 941
LENGTH: 1384
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; ORGANISM: HOMO
US-09-338-467-941
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                               tctctctggacaaagtcttccgggaacgggagtccctgaatgccagcattgtggatgcca
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Pred. No. 4.5e-277;
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                                                                                                        CURRENT APPLICATION NUMBER: US/09/644,869
CURRENT FILING DATE: 2000-08-28
PRIOR APPLICATION NUMBER: 60/151,062
PRIOR FILING DATE: 1999-08-27
NUMBER OF SEQ ID NOS: 9708
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8024
LENGTH: 1384
                                                                                                                                                                                                                                                                                                        Sequence 8024, Application US/09644869 GENERAL INFORMATION:
            Query Match
Best Local Similarity
Matches 1177; Conserv
                                                                        ORGANISM: HOMO
-09-644-869-8024
                                                                                                                                                                                                          APPLICANT: Holtzman, Douglas A. APPLICANT: Monahan, John APPLICANT: Richardson, Jennifer TITLE OF INVENTION: NOVEL NUCLEIC TITLE OF INVENTION: THEREFOR FILE REFERENCE: 1600.1182-001
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                     aagccccagtgccagggactccagactcactctccagtgggagcagcagagatgtccagg
                               AAGCCCCAGTGCCAGGACTCCAGACTCACTCTCCCAGTGGGAGCAGCAGAGATGTCCCAGG
                                                                                ACCCTGGCGATGTCACCAGCATGGTGGCTCAGGCCATGGGTGTATATGGAGCCCTCACCA
                                                                                                                                 AGTATGTCAGCGCGTTCTCCAAACTGGCCAAGGACTCCAACACTATCCTACTGCCCTCCA
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                                                                     accetggegatgteaceageatggtggeteaggeeatgggtgtatatggageeeteacea
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; LENGTH: 1384
; TYPE: DNA
; ORGANISM: HOMO :
US-09-649-162-7309
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TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.1181-001
CURRENT APPLICATION NUMBER: US/09/649,162
CURRENT FILING DATE: 2000-08-28
PRIOR APPLICATION NUMBER: 60/151,057
PRIOR APPLICATION NUMBER: 60/151,057
PRIOR FILING DATE: 1999-08-27
NUMBER OF SEG ID NOS: 9990
SOFTWARE: FASUSEQ for Windows Version 4.0
SEG ID NO 7309
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US-09-649-162-7309
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Best Local Similarity 99.4%;
Matches 1177; Conservative
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                                         tctctctggacaaagtcttccgggaacgggagtccctgaatgccagcattgtggatgcca
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Richardson, Jennifer
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Pred. No. 4.5e-277;
0; Mismatches 5;
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SEQ ID NO 7925
LENGTH: 1384
TYPE: DNA
ORGANISM: Homo S
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Best Local Similarity
Matches 1177; Conserv
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                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS:
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GENERAL INFORMATION:
APPLICANT: MCCarthy, Sean A.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MC
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.1180-001
CURRENT APPLICATION NUMBER: US/09/652,109
CURRENT FILING DATE: 2000-08-30
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GCTGGCGCGCGCGGCGGGGGCCCTGGGGCCCTTTTTGCTGAGGGGCTCTCTACTGGCTT 125
                                          ctgggagcgaccgctccgctcgtctcgttggttccggaggtcgctgcggcggtgggaaat 63
                                                                 CTGGGAGCNACCGCTCCGCTCGTCTCGTTGGTTCCGGAGGTCGCTGCGGCGGCGGTGGGAAAT 65
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                                                                                                                                           Score 1155; DB 25; Pred. No. 4.5e-277; 0; Mismatches 5;
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GENERAL INFORMATION:
APPLICANT: Shyjan, Andrew W.
TITLE OF INVENTION: NOVEL NUCLEIC ACID N
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.1183-001
CURRENT APPLICATION NUMBER: US/09/652,127
CURRENT FILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: 60/151,134
PRIOR APPLICATION NUMBER: 1999-08-30
VINMBER OF SEQ ID NOS: 10475
SOFTWARE: FastSEQ for Windows Version 4.
SEQ ID NO 7358
LENGTH: 1384
TYPE: DNA
ORGANISM: Homo sapiens
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                             atgtgccaccccgggtgaaagagtctatgcagatgcaggtggaggcagagcggcagaaac
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APPLICANT: Gutlerrez-Ramos, Jose-Carlos
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AN
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.1177-001
CURRENT APPLICATION NUMBER: US/09/652,816
CURRENT FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/152,111
PRIOR APPLICATION NUMBER: 60/152,111
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 9647
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7419
LENGTH: 1384
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GENERAL INFORMATION:
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TYPE: DNA
ORGANISM: HOMO
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                             gtacagatgcaagtcttgatgaggaacttgatcgagtcaagatgagttagtggagctggg
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RESULT 14
US-09-652-913-8809
; Sequence 8809, Application US/09652913
; GENERAL INFORMATION:

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TYPE: DNA
ORGANISM: HOMO
S-09-652-913-8809
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SOFTWARE: FastSEQ fo.
SEQ ID NO 8809
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Best Local Similarity
Matches 1177; Conserv
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CURRENT APPLICATION NUMBER: US/09/652,913
CURRENT FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/152,107
PRIOR FILING DATE: 1999-08-31
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TITLE OF INVENTION: THEREFOR
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600:1174-001
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Pred. No. 4.5e-277;
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Sequence 7997, Application US/09652914
GENERAL INFORMATION:
APPLICANT: Shyjan, Andrew W.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLE
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.1193-001
CURRENT APPLICATION NUMBER: US/09/652,914
CURRENT FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/152,112
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 9677
SOFTWARE: FastSEQ for Windows Version 4.0
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SEQ ID NO 7997
LENGTH: 1384
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Best Local Similarity
Matches 1177; Conserv
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NOVEL NUCLEIC ACID MOLECULES
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                                                   GTACAGATGCAAGTNTTGATGAGGAACTTGATCGAGTCAAGATGAGTTAGTGGAGCTGGG 1144
                                                                                  AAGCCCCAGTGCCAGGGACTCCAGACTCTCTCCAGTGGGAGCAGCAGAGATGTCCAGG 1084
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cttggccagggagtctggggacaaggaagcagattttcctgatt 1186
                                        gtacagatgcaagtcttgatgaggaacttgatcgagtcaagatgagttagtggagctggg
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Search completed: Job time: 6835 sec September 22, 2002, 16:14:40

on:

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Copyright (c) 1993 - 2000 Compugen Ltd
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/cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
/cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
/cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
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US-10-219-793-45
US-09-629-469A-11009
US-10-119-428-37
US-09-705-256A-3468
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US-09-1198-846-13409
PCT-US01-43704-1161
US-10-091-105-1428
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Sequence 18465, A	Sequence 29396, A	Sequence 7770, Ap	Sequence 8142, Ap	Sequence 15714, A	Sequence 30091, A	Sequence 688, App	Sequence 2445, Ap	Sequence 26126, A	Sequence 4825, Ap	Sequence 14079, A	Sequence 17868, A	Sequence 37723, A	Sequence 28244, A	Sequence 21791, A	Sequence 8693, Ap	Sequence 9558, Ap	Sequence 6734, Ap	Sequence 26, Appl	Sequence 26, Appl

## ALIGNMENTS

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; SEQUENCE DESCRIPTION: SEQ ID NO: US-09-898-216-2
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                                                                                                                                                                                                                            TELEX: <Unknown> INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/898,216
FILING DATE: 02-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/781,562
FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: NOVEL HUMAN MEMBRANE PROTEIN NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                       IMMEDIATE SOURCE:
                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: CA
COUNTRY: USA
ZIP: 94304
                                                                                                          LENGTH: 1188 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                       NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0181 US
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Query Best I

Match Local Similarity

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                                TCCAACCCTGGCGATGTCACCAGCATGGTGGCTCAGGCCCATGGGTGTATATGGAGCCCTC
                                                                         GAGCAGTATGTCAGCGCGTTCTCCAAACTGGCCAAGGACTCCAACACTATCCTACTGCCC
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ACCAAAGCCCCAGTGCCAGGGACTCCAGACTCACTCTCCAGTGGGAGCAGCAGAGATGTC
                                                               GAGCAGTATGTCAGCGCGTTCTCCAAACTGGCCAAGGACTCCAACACTATCCTACTGCCC
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                     {	t TCCAACCCTGGCGATGTCACCAGCATGGTGGCTCAGGCCATGGGTGTATATGGAGCCCTC}
                                                                                                         99.6%; Score 1183; DB 5;
larity 100.0%; Pred. No. 1.9e-289;
Conservative 0; Mismatches 0;
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             CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: 09/209, 462
PRIOR TILING DATE: 1998-02-11
PRIOR APPLICATION NUMBER: 60/049, 547
PRIOR FILING DATE: 1997-06-13
PRIOR APPLICATION NUMBER: 60/049, 547
PRIOR FILING DATE: 1997-06-13
PRIOR APPLICATION NUMBER: 60/049, 549
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PRIOR APPLICATION NUMBER: 60/049, 560
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PRIOR APPLICATION NUMBER: 60/049, 610
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PRIOR APPLICATION NUMBER: 60/049, 610
PRIOR FILING DATE: 1997-06-13
PRIOR APPLICATION NUMBER: 60/049, 611
PRIOR PRIOR APPLICATION NUMBER: 60/052, 989
PRIOR APPLICATION NUMBER: 60/052, 989
PRIOR FILING DATE: 1997-06-13
PRIOR APPLICATION NUMBER: 60/052, 989
PRIOR FILING DATE: 1997-06-13
PRIOR APPLICATION NUMBER: 60/052, 989
PRIOR FILING DATE: 1997-06-13
PRIOR APPLICATION NUMBER: 60/053, 966
PRIOR PRICING DATE: 1997-09-12
PRIOR APPLICATION NUMBER: 60/058, 669
PRIOR FILING DATE: 1997-09-12
PRIOR APPLICATION NUMBER: 60/058, 669
PRIOR PRICING DATE: 1997-09-12
PRIOR APPLICATION NUMBER: 60/058, 669
PRIOR FILING DATE: 1997-09-12
PRIOR APPLICATION NUMBER: 60/058, 971
PRIOR PRICING DATE: 1997-09-12
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CURRENT APPLICATION NUMBER: US/10/219,793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Rosen et al. TITLE OF INVENTION: 86
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DR FILING DATE: 1997-10-02

R APPLICATION NUMBER: 60/06

R FILING DATE: 1997-10-02
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SOFTWARE: PatentIn Ver.
SEQ ID NO 106
LENGTH: 1322
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Best Local Similarity
Matches 1177; Conserv
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LOCATION: (1322)
OTHER INFORMATION: n
-10-219-793-106
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PRIOR FILING DATE: 1997-10-02
PRIOR APPLICATION NUMBER: 60/061,059
PRIOR FILING DATE: 1997-10-02
PRIOR APPLICATION NUMBER: 60/061,060
PRIOR FILING DATE: 1997-10-02
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LOCATION: (1320)
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              ACTCTCTNTGGACAAAGTCTTCCGGGAACGGGAGTCCCTGAATGCCAGCATTGTGGATGC
                                                                       GGACCCTGAGTATGCCGTCACCCAGCTAGCTCAAACAACCATGAGATCAGAGCTCGGCAA 482
                                                                                                                                AATCGATGGAGTCCTTTACCTGCGCATCATGGACCCTTACAAGGCAAGCTACGGTGTGGA 422
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actctctctggacaaagtcttccgggaacgggagtccctgaatgccagcattgtggatgc
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; LOCATION: 1, 2, 1909, 19
; OTHER INFORMATION: n = A
US-10-198-846-12975
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US-10-198-846-12975
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                                                                                                                                           SOFTWARE: FastSEQ for Windows SEQ ID NO 12975
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12975, Application US/10198846 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                APPLICANT: Lillie, James
APPLICANT: Xu, Yongyao
APPLICANT: Wang, Youzhen
APPLICANT: Wang, Youzhen
APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS,
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT,
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
                                                                                  TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                            LENGTH: 1910
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                        CCAACCCTGGCGATGTCACCAGCATGGTGGCTCAGGCCATGGGTGTATATGGAGCCCTCA
                                                agcagtatgtcagcgcttctccaaactggccaaggactccaacactatcctactgccct
                                                             AGCAGTATGTCAGCGCGTTCTCCAAACTGGCCAAGGACTCCAACACTATCCTACTGCCCT
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Pred. No. 1.1e
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APPLICANT: Endege, Wilson
APPLICANT: Endege, Wilson
APPLICANT: Endege, Wilson
APPLICANT: Monahan, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THEI
FILE OF INVENTION: HUMAN PROSTATE CANCER
FILE OF INVENTION: HUMAN PROSTATE CANCER
FILE OF INVENTION NUMBER: US/09/785,276A
CURRENT APPLICATION NUMBER: 00.1-02-16
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR APPLICATION NUMBER: 60/183,862
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: 60/183,862
PRIOR APPLICATION NUMBER: 60/213,314
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR FILING DATE: 2000-06-09
PRIOR TILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 60/255,281
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; LOCATION: 1841, 1842
; OTHER INFORMATION: n =
US-09-785-276A-24973
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US-09-785-276A-24973
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GENERAL INFORMATION
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SOFTWARE: FastSEQ for Windows
SEQ ID NO 24973
LENGTH: 1842
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Best Local Similarity
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TYPE: DNA
ORGANISM: Homo:
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TGGAGCCTGGTTTGAACATCCTCATCCCTGTGTTAGACCGGATCCGATATGTGCAGAGTC
                                                          tgttcgtgccgcagcaggaggcctgggtggtggagcgaatgggccgattccaccggatcc
                                                                               TGTTCGTGCCGCAGCAGGAGGCCTGGGTGGTGGAGCGAATGGGCCGATTCCACCGGATCC
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Pred. No. 5.46
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RESULT 5
US-10-219-793-45

Sequence 45, Application US/10219793

GENERAL INFORMATION:
APPLICANT: ROSen et al.
TITLE OF INVENTION: 86 Human Secreted Protei.
FILE REFERENCE: P2008P101
CURRENT APPLICATION NUMBER: US/10/219,793
CURRENT FILING DATE: 2002-08-16
CURRENT FILING DATE: 0027-08-16
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CTGGGGCCCTTTTGCTGAGGGCCTCTCTACTGGCTTCTGGCCGCGCCTCCG-GCCGCCCT

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APPLICANT: ONSURI, TETSUJI
FILE OF INVENTION: PRIMERS FOR SYNTHESIZING FUI
FILE REFERENCE: 084335/0123
CURRENT APPLICATION NUMBER: US/09/629,469A
CURRENT FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: JP 1999-248036
PRIOR FILING DATE: 1999-07-29
PRIOR PRILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: JP 2000-118776
PRIOR APPLICATION NUMBER: JP 2000-183767
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: JP 2000-241899
PRIOR APPLICATION NUMBER: JP 2000-241899
PRIOR APPLICATION NUMBER: JP 2000-241899
PRIOR APPLICATION NUMBER: 60/159,590
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 60/183,322
PRIOR STILING DATE: 2000-02-17
NUMBER OF SEQ ID NOS: 19025
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                                                                                                               ; NAME/KEY: CDS
; LOCATION: (35)..(1102)
US-09-629-469A-11009
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APPLICANT: ISOCAL, TAKA
APPLICANT: NISHIKAWA, TA
APPLICANT: HAYASHI, KOJ
APPLICANT: SAITO, KAORU
APPLICANT: YAMAMOTO, JU
APPLICANT: ISHII, SHIZU
Query Match
Best Local Similarity
Matches 1153; Conserv
                                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver.
SEQ ID NO 11009
LENGTH: 1244
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                                                                                                                                                                                                                       TYPE: DNA
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                                                                                                                                                                                                  ORGANISM: Homo
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WAKAMATSU, AI
NAGAI, KEIICHI
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YAMAMOTO, JUNICHI
ISHII, SHIZUKO
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Score 1130.4; DB 5; Pred. No. 3.9e-276; 0; Mismatches 5;
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                                                     AACTTGAGTCAAGATGAGTTAGTGGAGCTGGGCTTNGCCAGGGAGTCTGGGGACAA 1168
                                                                                                                ACTCACTCTCCAGTGGGAGCAGCAGAGATGTCCAGGGTACAGATGCAAGTNTTGATGAGG
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Best Local Similarity
Matches 1128; Conserv
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APPLICANT:
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            gcaaatcgatggagtcctttacctgcgcatcatggacccttacaaggcaagctacggtgt
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (75)..(9098)
US-10-119-428-37
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TITLE OF INVENTION: NOVel Nucleic Acids
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 789CIP2
CURRENT APPLICATION NUMBER: US/10/119,42
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 09/596,193
PRIOR FILING DATE: 2000-06-17
PRIOR FILING DATE: 2000-06-17
PRIOR APPLICATION NUMBER: 09/574,454
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: 09/519,705
PRIOR APPLICATION NUMBER: 09/519,705
PRIOR APPLICATION NUMBER: 09/519,705
PRIOR APPLICATION NUMBER: 09/519,705
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: 09/519,705
PRIOR FILING DATE: 5000-03-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: pt_FL_genes Version SEQ ID NO 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS:
gttcgtgccgcagcaggaggcctgggtggtggagcgaatgggccgattccaccggatcct
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Ma, Yunging
Zhou, Ping
Zhao, Qing A.
Zhao, Yonghong
Yang, Yonghong
Drmanac, Radoje
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Asundi, Vinod
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orman, Tom
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Pred. No. 1.76
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Gaps

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RESULT 8
US-09-705-256A-3468
S Sequence 3468, App.
GENERAL INFORMATIO:
APPLICANT: Ma, Xi.
                                                                                                           APPLICANT: Ma, Xiao-Jun; Dotson, Stanton B.: Mon.
TITLE OF INVENTION: Tumor Associated Molecules (T.
TITLE OF INVENTION: and prevention of cancer
FILE REFERENCE: 3214
CURRENT APPLICATION NUMBER: US/09/705,256A
CURRENT FILING DATE: 199-05-11
PRIOR APPLICATION NUMBER: US 60/164,285
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 8259
SEQ ID NO 3468
                                                                     so:
                                                                                                                                                                                                                                                                                                                                      日
                                                                                                                                                                                                                         Sequence 3468, Application US/09705256A GENERAL INFORMATION:
            Query Match
Best Local Similarity
Matches 1131; Conserv
                                                                   TYPE: DNA
ORGANISM: Homo:
-09-705-256A-3468
                                                                                                  20 ID NO 3468
LENGTH: 1234
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                                AGCAGAGATGTCCAGGGTACAGATGCAAGTNTTGATGAGGAACTTTGATCGAGTCAAGATG
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PRIOR FILING DATE: FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: APPLICATION NUMBER: US
PRIOR FILING DATE: FILING DATE: 1998-02-13
NUMBER OF SEO ID NOS: 13203
SOFTWARE: FastSEO for Windows Version 3.0
SEO ID NO 11863
LENGTH: 1309
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Best Local
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ORGANISM: Homo sapiens
-09-919-002-11863
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APPLICANT: Liu, Jin
TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS CDNA
TITLE OF INVENTION: LIBRARIES
FILE REFERENCE: 20411-752CON1
CURRENT APPLICATION NUMBER: US/09/919,002
CURRENT FILING DATE: 2001-07-30
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PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FastSEQ for Windows Version (SEQ ID NO 13409
LENGTH: 1150
TYPE: DNA
ORGANISM: Homo sapiens
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Matches
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APPLICANT: Xu, Yongyao
APPLICANT: Wang, Youzhen
APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, ITITLE OF INVENTION: THERAPY OF BREAST CANCER
TITLE OF INVENTION: THERAPY OF BREAST CANCER
                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT FILING DATE: 2002-07-18
                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: THERAPY FILE REFERENCE: MRI-049
                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: 1149, 1150
OTHER INFORMATION: n = A,T,C
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            CGTGCCTGAGGAGTCGGCTGTGACTCTCGACAATGTAACTCTGCAAATCGATGGAGTCCT 377
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cggggctgagcagtcggctgtgactctcgacaatgtaactctgcaaatcgatggagtcct 166
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                                                           Conservative
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97.9%;
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                                                                                                                                                                                                                                                                            Version
                                                           Score 815.6;
Pred. No. 1.86
0; Mismatches
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                                                           1.8e-196;
ches 13;
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Sequence 1161, Application PC/TUS0143704

GENERAL INFORMATION:
APPLICANY: Corixa Corporation
APPLICANY: Stolk, John A.
APPLICANY: Stolk, John A.
APPLICANY: Stolk, John A.
APPLICANY: Mengher, Madelein Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: DIAGNOSIS OF COLON CANCI
FILE REFERENCE: 210121.561PC
COURRENT FILING DATE: 2001-11-19
NUMBER OF SEQ ID NOS: 2606
SOFTWARE: Corixa Invention Disclosure Patchers
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Sequence 2995, Application U.
GENERAL INFORMATION:
APPLICANT: Jiang, Yuqiu
APPLICANT: Chenault, Ruth,
APPLICANT: Todirias, Carol,
APPLICANT: Lodes, Michael,
APPLICANT: Secrist, Heathe,
APPLICANT: Carter, Darrick
APPLICANT: Smith, Carole L
APPLICANT: Smith, Carole L

Indirias, Carol Yoseph

Ruth

US/10214403

Lodes, Michael J.
Secrist, Heather
Carter, Darrick
Fanger, Gary R.
Smith, Carole L.

RESULT 12 US-10-214-403-2995/c

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LENGTH: 622
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 615
OTHER INFORMATION: n = A
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CAGGCCCAGATCCTGGCCTCCGAAGCAGAAAAGGCTGAACAGATAAATCAGGCAGCAGGA
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                                                                      GAGGCCAGTGCAGTTCTGGCGAAGGCCAAGGCTAAAGCTGAAGCTATTCGAATCCTGGCT
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                                  Conservative
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Pred. No. 1.1e-146;
1; Mismatches 3;
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; FEATURE:
NAME/KEY: misc_feature
LOCATION: 411
OTHER INFORMATION: n =
US-10-214-403-2995
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CURRENT APPLICATION NUMBER: U$710/214,403
CURRENT FILING DATE: 2007-08-06
NUMBER OF SEQ ID NOS: 3420
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2995
LENGTH: 550
TYPE: DNA
                                                 Sequence 58, Application PC/TUS0143704 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 547; Conserv
APPLICANT: Corixa Corporation APPLICANT: Stolk, John A. APPLICANT: Xu, Jiangchun APPLICANT: Chenault, Ruth A.
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                                                                                                                            TGTCCAGGGT
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LENGTH: 563
TYPE: DNA
ORGANISM: Homo s
PCT-US01-43704-58
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CURRENT APPLICATION NUMBER: PCT/US01/43704
CURRENT FILING DATE: 2001-11-19
NUMBER OF SEQ ID NOS: 2606
SOFTWARE: Corixa Invention Disclosure Database
SEQ ID NO 58
LENGTH: 563
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                                                                                                                                                     RESULT
                                                                                                            Sequence 1428, Application US/10097105 GENERAL INFORMATION:
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Best Local Similarity
APPLICANT: Meagher, Madeleine Joy
APPLICANT: King, Gordon E.
APPLICANT: Secrist, Heather
APPLICANT: Harlocker, Susan L.
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCE
FILE REFERENCE: 210121.504C1
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APPLICATION

NUMBER: US/10/097,105

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| LENGTH: 691
| TYPE: DNA
| ORGANISM: Homo sapiens
| FEATURE:
| NAME/KEY: misc_feature
| LOCATION: 439, 508, 523, 526, 539, 56
| LOCATION: 626, 645, 648, 664
| OTHER INFORMATION: n = A,T,C or G
| US-10-097-105-1428
RESULT 15
US-09-629-469A-1950
; Sequence 1950, Application US/09629469A
; GENERAL INFORMATION:
; APPLICANT: OTA, TOSHIO
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NUMBER OF SEQ ID NOS: 1562
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 1428
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Best Local Similarity
Matches 616; Conserv
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                                                                                                                     gtgnacttttacca
                                                                                                                                               CTGCAGCTCTGACA 861
                                                                                                                                                                                        AG-AGGCCAGTGCAGTTCTGGCGAAGGCCAAGGCTAAAGCTGAAGCTATTCGAATCCTGG
                                                                                                                                                                                                                                                                                                     TAGAGTCTGAGGGGACCCGAGAGTCGGCCATCAATGTGGCAGAAGG-----GAAGAAACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCACCCAGCTAGCTCAAACAACCATGAGATCAGAGCTCGGCAAACTCTCTNTGGACAAAG
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                                                                                                                                                                           anaagcccattgcngtttttgcnaangccaaggttaaaaactgaanctnttcgaatcctgg
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Pred. No. 7.4e-121;
0; Mismatches 46;
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CURRENT APPLICATION NUMBER: US/09/629,469A
CURRENT FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: JP 1999-248036
PRIOR FILING DATE: 1999-07-29
PRIOR PILING DATE: 1999-08-27
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: JP 2000-118776
PRIOR APPLICATION NUMBER: JP 2000-183767
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: JP 2000-183767
PRIOR FILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: JP 2000-241899
PRIOR APPLICATION NUMBER: G0/159,590
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: 60/159,590
PRIOR FILING DATE: 1999-10-18
PRIOR FILING DATE: 1999-10-18
PRIOR FILING DATE: 1999-10-18
PRIOR FILING DATE: 2000-02-17
NUMBER OF SED ID NOS: 19025
SOFTWARE: PATENTIN VET. 2.1
SED ID NO 1950
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TITLE OF INVENTION: PRIMERS FOR SYNTHESIZING FULL-LENGTH CDNA AND THEIR USE
FILE REFERENCE: 084335/0123
                                                                                              NAME/KEY: misc_feature LOCATION: (508)..(508) OTHER INFORMATION: "n"
                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature LOCATION: (426)..(426) OTHER INFORMATION: "n"
                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature LOCATION: (333)..(333) OTHER INFORMATION: "n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature LOCATION: (258)..(258) OTHER INFORMATION: "n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Homo sapiens FEATURE:
                         NAME/KEY: misc_feature
LOCATION: (533). (533)
OTHER INFORMATION: "n"
FEATURE:
                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: (445)..(445)
OTHER INFORMATION: "n"
                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: (441)..(441)
OTHER INFORMATION: "n"
                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature LOCATION: (438)..(438) OTHER INFORMATION: "n"
                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: (379)..(379)
OTHER INFORMATION: "n"
                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE
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NAME/KEY: misc_feature LOCATION: (561). (561)
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SUGIYAMA, TOMOYASU
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## ALIGNMENTS

RESULT AF161458

source	FEATURES	JOURNAL	AUTHORS	REFERENCE	TITLE	AUTHORS	REFERENCE	MEDLINE	JOURNAL		TITLE		REFERENCE		ORGANISM	SOURCE	KEYWORDS	ACCESSION	DEFINITION	Locus
11218 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="cBCAPB12" /cell_type="cd34+ stem cells" /tissue_type="blood"	Location/Qualifiers	Direct Submission  Submitted (23-JUN-1999) Shanghai Institute of Hematology, Shanghai Second Medical University, Rui-Jin Hospital, 197 Rui-Jin Road II,	Ye,M., Zhang,Q.H., Zhou,J., Shen,Y., Wu,X.Y., Guan,Z.Q., Wang,L., Fan,H.Y., Mao,Y.F., Dai,M., Huang,Q.H., Chen,S.J. and Chen,Z.	3 (bases 1 to 1218)	Human full length cDNA cloned from cd34+ stem cells	Ye,M., Zhang,Q.H., Zhou,J., Shen,Y., Wu,X.Y., Guan,Z.Q., Wang,L., Fan,H.Y., Mao,Y.F., Dai,M., Huang,Q.H., Chen,S.J. and Chen,Z.	2 (bases 1 to 1218)	20499367	Genome Res. 10 (10), 1546-1560 (2000)	<pre>ior 300 previously underlined genes expressed in CD34+ nemacopoletic stem/progenitor cells</pre>	Cloning and functional analysis of cDNAs with open reading frames	Shen, Y., Fan, H.Y., Lu, G., Zhong, M., Xu, X.R., Han, Z.G., Zhang, J.W.,	1 (bases 1 to 1218)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		human	HTC.	AFI61458 1 CT.6841430	iens HSPC108 mRNA, complete cds.	AF161458 1218 bp mRNA linear HTC 22-MAY-2001

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//product="GI:6841440"
//db_xref="GI:6841440"
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//translation="mrgSLLASGRACRASSGLPRNTVVLFVPQQEAWVVERMGREHRI
//translatidpvLDRIRYVOSLKEIVINVPEQSAVTLONVTLQIDGVLYLRIMDPYKAS
YGVEDPEYAVTQLAQTTMRSELGKLSLDKVFRERESLNASIVDAINQAADCWGIRCLR
YEIKDIHVPENVESMOMQVEAERKETVLESSGTRESAINVAEGKKOAQILASEAE
KAEQINQAAGEASAVLAKAKAKAEAIRILAAALTQHNCDAAASLTVAEQYVSAFSKLA
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GCAGCAGGAGGCCTGGGTGGAGCGAATGGGCCGATTCCACCGGATCCTGGAGCCTGG
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1 (bases 1 to 935)
Li,W.B., Gruber,C., Jessee,J.
Full-length cDNA libraries and
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , mRNA sequence. AL541792 AL541792.1 GI:1
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AL541792 LTI_FL002_PL1 Homo s
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BP 191 91006 EVRY. cedex - France
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                                                    Conservative
                                                                                                                             /note="Organ: placenta; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com" 4 others
                                                                                                                                                                                                                                                                                                                                                                    segref@genoscope.cns.fr,
Location/Qualifiers
                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CSODE007YE18"
/clone_lib="LTI_FL002_PL1"
/lab_host="DH10B"
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                     BM476304
AGENCOURT_6479118 N
5', mRNA sequence.
BM476304
BM476304.1 GI:1852
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human.
Homo sapiens
Eukaryota; Metazoa;
Mammalia; Eutheria;
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NIH_MGC_88
Chordata;
Primates;
                                                        Homo
Craniata; Vertebrata; Catarrhini; Hominidae
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Plate: LLAM12282 row: k column: 20
High quality sequence start: 8
High quality sequence stop: 678.
Location/Qualifiers
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Tissue Procurement: ATCC
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National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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//db xref="taxon:9606"
//db xref="taxon:9606"
//clone="IMAGE:5558923"
//clone_lib="NIH_MGC_88"
//tissue_type="duodenal adenocarcinoma, cell line"
//lab_host="DH108 (phage-resistant)"
//note="Organ: small intestine; Vector: pCMV-SPORT6;
Site_1: NotI; Site_2: SalI; Cloned unidirectionally;
oligo-dT primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NIH_MGC Library."
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AL516503 LTI_NFL011_NBC1
prime, mRNA sequence.
                                                                                                                                                                                 Contact: Genoscope
Genoscope - Centre National
BP 191 91006 EVRY cedex - FJ
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Full-length cDNA libraries
Unpublished (2001)
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Mammalia; Eutheria;
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(bases 1 to 962)
                                                                                                                                                                       segref@genoscope.cns.fr,
       /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library is not normalized, but is the control for the normalized libraries. Library was constructed by Life morphological primers.
                                                                                                     /clone="CSODA006YH04"
/clone_lib="LTI_NFL011_NBC1"
                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                         /tissue_type="neuroblastoma cells"
/lab_host="DH10B"
                                                                                             /sex="male"
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                CAATGTAACTCTGCAAATCGATGGAGTCCTTTACCTGCGCATCATGGACCCTTACAAGGC
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5', mRNA sequence.
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National Institutes of Health, Mammalian
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/clone_lib="NIH_MGC_72"
/tissue_type="melanotic melanoma"
/lab_host="DH108 (phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo careage insert size 2 kb. Library constructed by Life Technologies."

276 c 292 g 194 t 7 others
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/db_xref="taxon:9606"
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5', mRNA sequence.
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                                                         CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM12332 row: 1 column: 06
                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, N
                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
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/lab_host="DHIOB (phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Si
/note="Organ: skin; Vector: pCMV-SPORT6; Si
/site_2: Sall; Cloned unidirectionally. Pri
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RRS Adachi, J., Alzawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Adachi, J., Alzawa, K., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Hume, D., Imotani, K., Ishi, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Nunazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J., Salto, H., Satio, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Schriml, L., Shibata, K., Shibata, Y., Shinagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yamanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yamanaka, T., Tanaka, T., Toyahida, K., Yoshino, M., Muramatsu, M. and
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Shibata,K.,
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AK002793
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Mus musculus (strain:C57BL/6J) adult male kidney cDNA to clone_lib:RIKEN full-length enriched mouse cDNA library
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tstrumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
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XhoI. Host: SOLR.
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/clone_lib="RIKEN full-length enriched mouse
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/strain="C57BL/6J"
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                                                  CCCAGCTAGCTCAAACAACCATGAGATCAGAGCTCGGCAAACTCTGTNTGGACAAAGTCT
                            GCTGGGGTATCCGCTGCCTNCGTTATGAGATCAAGGATATCCATGTGCCCACCCCGGGTGA
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CDNA Library Arrayed by: The I.M.A.G.E. Congortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lnl.gov
Plate: LLAM12137 row: n column: 16
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Tissue Procurement: ATCC
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National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
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Location/Qualifiers
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/site_2: SalI; Cloned unidirectionally. Primer: Oligo
Site_2: SalI; Cloned unidirectionally. Primer: Oligo
Average insert size 1.75 kb. Library constructed by
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1 (bases 1 to 849)

Li.W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished (2001)

Contact; Genoscope
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/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contact: Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax: (1) 301 610
8371 Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com"
1 others
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Eutheria;
Chordata; Craniata; Vertebrata; Primates; Catarrhini; Hominidae;
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                                             AGCTGAAGCTATTCGAATCCTGGCTGCAGCTCTGACACAACATAATGGAGATGCAGCAGC
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM12208 row: m column: 18 High quality sequence stop: 661.
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Tissue Procurement: ATCC
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Location/Qualifiers
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="IMAGE:5529785"
/clone="lib="NxH_MCC_71"
/tissue_type="leiomyosarcoma"
/tissue_type="leiomyosarcoma"
/lab_host="DHH10B (phage-resistant)"
/note="organ: uterus; Vector: pcMV-SPORT6; Si-
/note="organ: uterus; Vector: pcMV-SPORT6; Si-
/site_2: SalI; Cloned unidirectionally. Prime
Average insert size 2.1 kb. "
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www
Location/Qualifiers
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Full-length cDNA libraries
Unpublished (2001)
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AL525167
AL525167.1 GI:12788660
EST.
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Mammalia; Eutheria;
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                                                                                           Conservative
                                                                                                                                                                                         /tissue_type="neuroblastoma cells"
//lab_host="DH10B"
//lab_host="DH10B"
//note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
/note="Organ: brain; Vector: pCMVSPORT 6]
//note="Organ: brain; Vector: prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
/note of the pCMVSPORT 6
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/clone_lib="LTI_NFL003_NBC3"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                       67.6%;
94.2%;
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Primates;
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24; Mismatches
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Eukaryota; Metazoa; Chordata; Cri
Mammalia; Eutheria; Primates; Ca
1 (bases 1 to 1095)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mi
Unpublished (1999)
                                                                                                                                                                         1095
AGENCOURT_6402181 NIH_MGC_41
5', mRNA sequence.
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                                                                     Craniata; Vertebrata; Catarrhini; Hominidae
                     Mammalian
                                                                                                                                                                                                             sapiens
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1059

240 999 300 939 360

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480 759 540 699 600 639 660 579 720

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(MGC)

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TGGCCTCCGAAGCAGAAAAGGCTGAACAGATAAATCAGGCAGCAGGAGAGGCCCAGTGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, I
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plate: LLCM2017 row: b column: High quality sequence stop: 503.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="amelanotic melanoma, cell line"
//lab_host="DHIOB (phage-resistant)"
/note="Organ: skin; Vector: poTBT; Site_1: xhoI; Site_2:
EccRI; cDNA made by oligo-dT priming. Directionally cloned into EccRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NH_MGC Library."

282 c 302 g 226 t
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/clone="IMAGE:5516467"
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/db_xref="taxon:9606"
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TGTTCGTGCCGCAGCAGGAGGCCTGGGTGGTGGAGCGAATGGGCCGATTCCACCGGATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
Contact: Robert Strausberg,
                                                                   Similarity 97.3
36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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NIH-MGC http://mgc.nci.nih.gov,
National Institutes of Health,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Location/Qualifiers
                                                                                                                                                                /organism="Homo sapiens"
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/clone="IMAGE:5534403"
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/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Not Site_2: SalI; Cloned unidirectionally. Primer: Oligo Average insert size 2.1 kb. "
Average insert size 2.1 kb. "
3 others
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97.2%;
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                                                                                                     mRNA sequence.
BG479080
BG479080.1 GI
EST.
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
Unpublished (1999)
                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 943)
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IMAGE:4649846 5',
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 ATCCGCTGCCTNCGTTATGAGATCAAGGATATCCATGTGCCACCCCGGGTGAAAGAGTCT
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN
DNA Sequencing by: Incyte Genomics, Inc.

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov Plate: LLCM1430 row: e column: 15
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="choriocarcinoma"
//tab_host="pH108 (phage resistant)"
/lab_host="pH108 (phage resistant)"
/note="Organ: placenta; vector: pOTB7; Site_1: XhoI;
/note="Organ: placenta; vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by ling Hong in the laboratory of Gerald M. Rubin (University of Callifornia, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
a 254 c 290 g 189 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4649846"
/clone_lib="NIH_MGC_21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66.6%;
98.4%;
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Indels Length

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                   GTCCTTTACCTGCGCATCATGGACCCTTACAAGGCAAGCTACGGTGTGGAGGACCCCTGAG 432
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GAAGCAGAAAAGGCTGAACAGATAACTCAGGCAGCAGGAGAGGCCCAGTGCAGTTCTGGGC
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                                                                                  804;
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12019 row: n column: 24
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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1 (bases 1 to 920)
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National Institutes of Health, Mammalian
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                                                                                  Conservative
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                                                                                                                                                                                                                                  /clone="IMAGE:5400023"
/clone_lib="NIH_MGC_87"
/clone_lib="NIH_MGC_87"
/tissue_type="mammary adenocarcinoma, cell line"
/tissue_type="m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                        99.0%;
                                                                                0,
                                                                                                        Score 791.2;
Pred. No. 4e
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Search completed: September 22, 2002, 14:49:21 Job time: 5287 sec

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SEQUENCE 343 AA; 38
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P16756;
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STRAIN-LONG EVANS; TISSUE-Lung;
JONES M.L., Shanley T.P., Ward P.A.;
SUBMITTED (FEB-1994) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: CHEWOATTRACTANT FOR BLOOD MONOCYTES, MEMORY T
CELLS AND EOSINOPHILS. CAUSES THE RELEASE OF HISTAMINE F
BASOPHILS AND ACTIVATES EOSINOPHILS (BY SIMILARITY).
-I- SUBCELLULAR LOCATION: Secreted.
-I- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL
C-C) (CHEMOKINE CC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-90269039; PubMed-2161319; Chee M.S., Bankler A.T., Beck S., Bohni R., Brown C.M., Cerny R., Horsnell T., Hutchison C.A. III, Kouzarides T., Martignetti J.A., Preddle E., Satchwell S.C., Tomlinson P., Weston K.M., Barrell B.G.; "Analysis of the protein-cooling content of the sequence of human cytomegalovirus strain AD169.";
                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                        Rattus norvegicus (Rat).
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01-OCT-1996 (Rel.
15-JUL-1999 (Rel.
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HSSP; P04002; lATF.
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Viruses; dsDNA viruses, no RNA stag
Betaherpesvirinae; Cytomegalovirus.
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P05442;
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Rhodospirillum.
NCBI_TaxTD-101
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SEQUENCE
                                                                                 entities requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=85251588; PubMed=2861810;
Falk G., Hampe A., Walker J.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             epsilon subunit).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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InterPro; IPR001811; Chemokine_IL8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ralk G., Hampe A., Walker J.E.;
"Nucleotide sequence of the Rhodospirillum
Biochem. J. 228:391-407(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00472; SMALL_CYTOKINES_CC;
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SIMILARITY: BELONGS TO THE ATPASE EPSILON CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: Produces ATP from ADP in gradient across the membrane. CATALYTIC ACTIVITY: ATP + H(2)O +
                                                                                                                                                                                                           European
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: F-type atpases
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een the Swiss Institute of Bioinformatics and the EN
European Bioinformatics Institute. There are no resti
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                               X02499;
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There are no rest
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RL29_HUMAN
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MEDIJNR-96180309; PubMed-8597591;

Law P.T., Tsui S.K., Lam W.Y., Luk S.C., Hwang D.M., Liew C.C.,

Lee C.Y., Fung K.P., Waye M.M.;

"A novel cDNA encoding a human homologue of ribosomal protein L29.";

Biochim. Biophys. Acta 1305:105-108(1996).
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Pfam; PF02823; ATP-synt_DE.W; 1.
ProDom; PD000944; ATP-synt_DE; 1.
Hydrolase; ATP synthesis; CF(1); Hydrogen ion transport.
SEQUENCE 134 AA; 14307 MW; 8905084DF31C9222 CRC64;
                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                    MEDLINE=96216099; PubMed=8662616;
Liu S., Smith S.E., Julian J., Rohde L.H., Karin "cDNA cloning and expression of HIP, a novel cell sulfate/heparin-binding protein of human uterine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
60S_ribosomal protein L29 (Cell surface heparin binding
                                                                                                     EMBL; U10248; AAC50499.1; -. EMBL; Z49148; CAA89008.1; -. EMBL; U49083; AAC50647.1; -. MIM; 601832; -.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                 [NIT_MET
                                             Ribosomal protein;
                                                             roDom;
                                                                          Pfam; PF01779; Ribosomal_L29e;
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                                                                                                                                                                                                                                                                                                              Biol.
                                                                                                                                                                                                                                                                                          Biol. Chem. 271:11817-11823(1996).
SIMILARITY: BELONGS TO THE L29E FAMILY OF RIBOSOMAL PROTEINS
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 PD01779; Ribosomal_L29e; 1.

PD010314; Ribosomal_L29e; 1.

al protein; Repeat; Heparin-binding.

T 0 0 BY SIMILARITY.

T 119 119 R -> A (IN REF. 2).

E 158 AA; 17621 MW; 8FCC38682E6DDF28 CRC64;
                                                                                      IPR002673; Ribosomal_L29e.
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HIP, a novel cell surface heparan
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RESULT 7
K2C5_BOVIN
ID K2C5_B
AC P04262
DT 20-MAR
DT 20-MAR
DT 16-OCT
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K2C5_BOVIN
P04262;
20-MAR-1987
20-MAR-1987
16-OCT-2001
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Q9K6D6;
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BACHD
                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restuse by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus halodurans.
Bacteria; Firmicutes; Bacillus/Staphylococcus
NCBI_TaxID=86665;
                                                                                                                                                                                                                                                                                        modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Takami H., Nakasone K., Takaki Y., Maeno G., So
Fuji F., Hirama C., Nakamura Y., Ogasawara N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         factor).
RPOE OR BH3793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Probable DNA-directed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40,
16-OCT-2001 (Rel. 40,
16-OCT-2001 (Rel. 40,
                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                          DNA-directed
                                                                                                                                                                                                                                                        EMBL; AP001520; BAB07512.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20512582; PubMed=11058132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'Complete genome sequence of the alkaliphilic bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122
                                                                                                                                 250 KAKAKAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              249 AKAKAKA 255
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                                                                                                           86
                                                                                                                                                                                                                                                                             send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                         OF TRANSCRIPTION. IN THE PRESENCE OF THE DELTA SUBUNIT, RNAP DISPLAYS AN INCREASED SPECIFICITY OF TRANSCRIPTION, A DECREASED AFFINITY FOR NUCLEIC ACIDS, AND AN INCREASED EFFICIENCY OF RNA SYNTHESIS BECAUSE OF ENHANCED RECYCLING (BY SIMILARITY).

SUBUNIT: RNAP IS COMPOSED OF A CORE OF 2 ALPHA, A BETA AND A BETA SUBUNITS. THE CORE IS ASSOCIATED WITH A DELTA SUBUNITS AND ONE OF SEVERAL SIGMA FACTORS (BY SIMILARITY).

SIMILARITY: BELONGS TO THE RPOE FAMILY.
                                                                                                           KAKAKAE
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                                                                                                                                                                    Similarity
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(Rel.
(Rel.
                                                                                                                                                          Conservative
                                                                                                                                                                                                                  RNA polymerase; 1
104 164. I
64 AA; 19213 MW;
                                                                                                                                 256
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                                               STANDARD;
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100.0%;
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Created)
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RNA polymerase delta
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polymerase delta subunit (RNAP delta
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1; 26E91F666DE67C7A CRC64;
                                                                                                                                                                     Score 7;
Pred. No.
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Pred. No.
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Best Local Similarity
Matches 7; Conserv
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P76471;
15-DEC-1998
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SEQUENCE
 Mau |
"The
                  SEQUENCE FROM N.A.
STRAIN-KI2 / MG1655;
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A.
Riley M., Collado-Vides J., Glasner J.D.,
Gregor J., Davis N.W., Kirkpatrick H.A., C
                                                                                                                                                                                                                                                                                                                                                                                                 NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001664; IF. Pfam; PF00038; filament; 1. PROSITE; PS00226; IF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-85128114; PubMed-6084625;
Jorcano J.L., Franz J.K., Franke W.W.;
"Amino acid sequence diversity between bovine epidermal cytokeratin
polypeptides of the basic (type II) subfamily as determined from cDI
clones.";
                                                                                                                                             YFAZ OR B225
                                                                                                                                                                 15-DEC-1998
16-OCT-2001
                                                                                                                                                                                                                         ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; K03534; AAA30601.1; -. PIR; A02948; KRBO2B. HSSP; P10968; IWGC.
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Bovidae; Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Crania;
Mammalla; Eutheria; Cetartiodactyla;
                                                                                                             Escherichia
                                                                                                                     Bacteria; Proteobacteria;
                                                                                                                                Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                        Intermediate filament; Coiled coil; Keratin
                                                                                                                                                                                                                                                                    145
                                                                                                                                                                                                                                                                                        331 LSSGSSR 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 s SWISS-PROT entry is copyright. It is produced through a collal ween the Swiss Institute of Bioinformatics and the EMBL outs: European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in ified and this statement is not removed. Usage by and for continuous contents in the content is not removed.
           B.,
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complete
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166
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(Rel. 37, Last sequence update)
(Rel. 40, Last annotation update)
protein yfaz precursor.
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llarity 100.0%;
Conservative
genome
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166
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15505
sequence
                                                                                                                      gamma subdivision; Enterobacteriaceae;
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of
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Escherichia
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Ruminantia; Pe
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                     Goeden
                            Rode C.K., Mayhew G.F.
coli
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                   м. А.,
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K-12.";
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                     D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a collaboration
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RESULT 9
UREF_HAEIN
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Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                         SEQUENCE FROM M. ...

STRAIN=RD / KW20 / ATCC 51907;

STRAIN=RD / KW20 / ATCC 51907;

STRAIN=RD / KW20 / ATCC 51907;

Fleisohmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Fleisohmann R.D., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Fine L.D., Fritchman J.L., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions along as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                 modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
          InterPro; IPR002639; UreF.
Pfam; PF01730; UreF; 1.
ProDom; PD004961; UreF; 1.
                                                        EMBL; U32736; AAC22195.1; TIGR; HI0537; -.
                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Haemophilus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UREF_HAEIN P44395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein; SIGNAL 1 2
                                                                                                                                                                                                                                                         Science 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                    Venter J.C
                                                                                                                                                                                                                                                                       "Whole-genome
influenzae Rd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          328
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                                                                                                                                                 non-profit institutions as long
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1 POTENTIAL.
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Pred. No.
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                                                                                                                                                                                                                                                                                     assembly
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                                                                                               Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOLD_VIBCH
P57066;
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A., Gwinn M.L., Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D., Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P. McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=EL TOR N16961 /
                                                                                                                                                                                                 NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 406:477-483(2000).

-ir function: part of an arp-dependent transport system responsible for the release of Lipoproteins targeted to the Outer membrane from the inner membrane. Such a release is dependent of the Sorting-Signal (absence of an Asp at Position 2 of the Mature Lipoprotein) and of Lola (by Similarity).

-i- SUBCELLULAR LOCATION: Inner membrane-associated (by similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20406833; PubMed=10952301; Heidelberg J.F., Eisen J.A., Nelson W.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOLD OR VC1883.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VIBCH
                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE004263; AAF95031.1; -. TIGR; VC1883; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vibrio cholerae
                                                                                                                                                                                                                   ATP-binding; Transport; Complete proteome.
NP_BIND 41 48 ATP (BY SIMILARITY)
                                                                                                                                                                                                                                                                      SMART; SM00382; AAA; 1.
PROSITE; PS00211; ABC_TRANSPORTER; 1.
                                                                                                                                                                                                                                                                                                                  InterPro; IPR003593; AAA.
InterPro; IPR003439; ABC_tr:
InterPro; IPR001687; ATP_GT
Pfam; PF00005; ABC_tran; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "DNA sequence of both chromosomes of the cholera pathogen Vibrio
                            249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY:
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                       AKAKAKA
                                                                                               Similarity
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                                                                                                                                                                                                 228 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BELONGS TO THE ABC TRANSPORTER FAMILY. LOLD SUBFAMILY.
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                                                                                                                                                                                                 24890 MW;
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                                                                                                                                                                                                                                                                                                                                              ATP_GTP_A.
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                                                                                               100.0%;
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                                                                                               Score 7; Pred. N
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Pred. No
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                                                                                                                                                                                                 315E52CB775E61E6 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  subdivision; Vibrionaceae; Vibrio.
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27;
                                                                                               DB 1;
). 31;
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                                                                                                                      Length 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
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                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
FIXA_RHILP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                       01-FEB-1995 (Rel. 01-FEB-1995 
                                                                                                                                                                                                                                                                                                                     FIXA_RHILP
Q05559;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BACHD
                                                                                                                                           Rhizobium leguminosarum (biovar phaseoli).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA repair protein RADC OR BH3032.
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Michiels J.,
                                                SEQUENCE FROM N.A
                                                                                                                         Bacteria; Proteobacteria;
Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                     FixA protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProDom; PD007415; RadC; 1 PROSITE; PS01302; RADC; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00633; HHH; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000445; HHH. InterPro; IPR001405; RadC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AP001517; BAB06751.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of BioInformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   halodurans and genomic sequence comparison Nucleic Acids Res. 28:4317-4331(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Takami H., Nakasone K., Takaki Y., Maeno G., S
Fuji F., Hirama C., Nakamura Y., Ogasawara N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20512582; PubMed=11058132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=C-125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacillus/Staphylococcus
NCBI_TaxID=86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus halodurans
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                       MEDLINE=93379046; PubMed=8369342;
                                                                                               NCBI_TaxID=385;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA repair;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: BELONGS TO THE RADC FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Complete genome sequence of the alkaliphilic bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: INVOLVED IN DNA REPAIR (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                232 AA;
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Vanderleyden J.;
                                                                                                                   Rhizobium
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                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                          . 31, Created)
. 31, Last sequence. 31, Last annotation.
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26403 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 7; DB 1; Pred. No. 32; 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 232
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P19654;
O1-FEB-1991
O1-FEB-1991
O1-FEB-1991
                                                                                                                           This SW:
                                                                                                                                                               Sternberg N., Cohen G.;
"Genetic analysis of the lytic replicon of bacteriophage Pl. II.
"Genetic analysis of the lytic replicon of bacteriophage Pl. II.
Organization of replicon elements.";
J. Mol. Biol. 207:111-133(1989).
-I- FUNCTION: ESSENTIAL FOR L-REPLICON FUNCTION. NECESSARY FOR
INITIATION OF DNA REPLICATION FROM THE L-REPLICON (PROBABLE).
                                             modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Pfam; PF01012; ETF_beta; 1.
ProDom; PD003528; ETF_betta; 1.
PROSITE; PS01065; ETF_BETA; 1.
Electron transport; Nitrogen fixation
SEQUENCE 279 AA; 30083 MW; 6ACB3E
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                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                Structure and regulation of the lytic replicon of Mol. Biol. 207:135-149(1989).
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X15639; CAA33662.1;
X15638; CAA33656.1;
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7; Conserv
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(Rel. 17, Last sequence update)
(Rel. 17, Last annotation update)
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A ROLE IN A REDOX F
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-1998
15-JUL-1998
16-OCT-2001
PRIMTS; PR00100; AOTCASE.
PROSITE; PS00097; CARBAMOYLTRANSFERASE; FALSE_NEG.
PROSITE; PS00097; CARBAMOYLTRANSFERASE; FALSE_NEG.
PROSITE; PS00097; CARBAMOYLTRANSFERASE; FALSE_NEG.
PROSITE; PS00097; CARBAMOYLTRANSFERASE; FALSE_NEG.
SEQUENCE 307 AA; 34913 MW; DB043BC5A40EBB5D CRC64;
                                                                                                                                                                                  modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                          "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus."; Nature 390:364-370(1997).
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PIR; S04263; RLBPP1.
DNA replication.
SEQUENCE 281 AA; 30857 MW; F3C:
                                                                                                  InterPro; IPR002029; Carbmyltransf_asor
                                                                                                                                                                                                                                                                                                                  -1- SUBCELLULAR LOCATION: Cytoplasmic.
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Archaea; Euryarchaeota;
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                                                                PF00185; OTCace; 1. PF02729; OTCace_N; 1.
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AF1255; -.
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36, Last sequence update)
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Search completed: September 22, Job time: 294 sec
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                                                                                                                                            Query Match 2.0%; Score 7; DB 1; Best Local Similarity 100.0%; Pred. No. 45; Matches 7; Conservative 0; Mismatches
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7_SPIOL
IN37_SPIOL
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                                                                                                                                                                                                                          EMBL; X56963; CAA40283.1; -.

PIR; $14409; $14409.

InterPro; IPR000051; $AM_bind.

InterPro; IPR000033; ubiE_COQ5_methyltransf.

Pfam; PF01209; Ubie_methyltran; 1.

Chloroplast; Transit peptide; Inner membrane.

TRANSIT 1 21 CHLOROPLAST.

CHAIN 22 344 AA; 38976 MW; 555E53242B297D7C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "cDNA sequence and deduced amino acid sequence of the precursor of the 37-kDa inner envelope membrane polypeptide from spinach chloroplasts. Its transit peptide contains an amphiphilic alpha-helix as the only detectable structural element.";

Eur. J. Blochem. 195:361-368(1991).
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01-NOV-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
37 kDuinner envelope membrane protein, chloroplast precursor (E37).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 120-141 AND 236-240.
MEDLINE-91348205; PubMed-1879527;
Block M.A., Joyard J., Douce R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-91146572; PubMed-1997321;
Dreses-Werringtoer U., Fischer K., Wachter E., Link T.A.,
Fluegge U.J.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                envelope protein.";
                                                                                                248 LAKAKAK 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Purification and characterization of E37, a major chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=3562;
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SUBCELLULAR LOCATION: CHLOROPLAST INNER MEMBRANE.
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             2002, 18:37:12
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Result
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score
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Gapop 60.0 , Gapext 60.0
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T1205863
B71689
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A35148
T18493
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C96680
AG3259
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RESULT 2 T21562 T21562 hypothetical protein F30A10.5 - C; Species: Caenorhabditis elega C; Date: 15-Oct-1999 #sequence_r C; Accession: T21562 R; Barlow, K. submitted to the EMBL Data Libr A; Reference number: Z19442 A; Accession: T21562 A; Status: preliminary; translat A; Molecule type: DNA	314 315	194 195 254 255	Query Match Best Local Matches 15	A; Status: translate A; Molecule type: DN A; Residues: 1-357 A; Cross-references: C; Genetics: C; Genetics: A; Map position: 9 A; Introns: 2/3; 48/ C; Superfamily: eryt	RESULT 1 T02246 hypothetical protein pl.11659 C; Species: Homo sapiens (man) C; Date: 05-Mar-1999 #sequence C; Accession: T02246 R; Lamerdin, J.E.; McCready, P.; Christensen, M.; Georgescu, submitted to the EMBL Data Lib A; Authors: Duarte, S.; Lucas, A; Description: Sequence analys A; Reference number: Z14637 A. Access ion. Tn.7246		00000000000000000000000000000000000000
Caeno Caeno Caeno Oct-1: T21: C. the numbo numbo relim type:	SVYGAL        SVYGAL	/EAERRI         EAERRI          (AEAIR:	cch al Simil 152; C	: 3; bn -3	Al protei Homo sap Mar-1999 1: T02246 J.E.; M J.E.;		777777777777777777777777777777777777777
tein F3C rhabditi 999 #seq 562 EMBL Da er: Z194 562 inary; t	ΓKAPVPGT 	VEAERRKRATVLESE             VEAERRKRATVLESE VEAEAIRILAAALTQF              KAEAIRILAAALTQF	ilarity Conserva	ba Fba	lical protein Pl.  5: Homo sapiens  65-Mar 1999 *seq  ion: T02246  iin, J.E.; McCrea  itensen, M.; Geor  d to the EMBL Da  rs: buarte, S.; L.  ption: Sequence  ption: Sequence  ince number: Z146		00000000000000000000000000000000000000
AA10.5 - C .s elegans  uence_rev  ita Librar  42  xanslated	SSTSDda	SEGTRES	42.7 100. ative	from GB/EMBL/ AM> EMBL:AC004472; ; 82/1; 101/3; rocyte band 7	#Sequence_re #sequence_re Cready, P.M. Georgescu, A Georgescu, A L Data Libra Since analysis		164 166 175 183 187 187 187 194 207 209 210 210 211 215 228
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aenorḥ ision y, Oct	GVYGALTKAPVPGTPDSLSSGSSRDVQGTDAS	VEAERRKRATVLESEGTRESAINVAEGKKOAQI	Score 15 Pred. N 0; Misma	NID:g29	human ision 05 Skowron ; Avila, y, March Bruce, of a hum	ALIGNMENTS	A84124 KRBO2B S43815 C97295 H64995 B91021 A85865 F64075 F63148 T17294 T17294 J74683 B75372 C82556 AE0793 A82147
abditis elegans 15-Oct-1999 #text_change 21-Jan-2000 Ober 1996 GB/EMBL/DDBJ	345 346	SEGTRESAINVAEGKKOAQILASEAEKAEQINQAAGEASAVLAKAKA 253	12; DB 2; Length 357; 10. 4.9e-142; 1tches 0; Indels 0; Gaps 0;	g2984582; PIDN:AAC07983.1; PID:g2984585 3; 194/3; 243/1; 269/3; 312/3	Mar-1999 #text_change 11-Jan-2000 .ski, E.; Adamson, A.W.; Burkhart-Schultz, K. J.; Liu, S.; Attix, C.; Andreise, T.; Trank , 1998 R.; Thomas, P.; Quan, G.; Kronmiller, B.; Ar an P1 clone containing the XRCC9 DNA repair	ENTS	DNA-directed RNA p keratin, 68K type hypothetical prote stage V sporulatio hypothetical prote procell receptor ga hypothetical prote hypothetical protein

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C:Genetics:
A;Gene: Rp328
C;Superfamily: erythrocyte band 7 integral membrane
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A;Cross-references: EMBL:Z81072; PIDN:CAB03018.1; GSPDB:GN00019; CESP:F30A10.5
A;Experimental source: clone F30A10
C;Genetics:
A;Gene: CESP:F30A10.5
A;Anap position: 1
A;Introns: 16/2; 68/3; 124/3; 227/2
C;Superfamily: erythrocyte band 7 integral membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-515 <BEV>
A;Cross-references: EMBL:AL035602
A;Experimental source: cultivar Columbia;
C;Genetics:
                                                                                                                                                                                                                                                                                C;Accession: B71689
R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark,
Nature 396, 133-140, 1998
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B71689
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A; Introns: 52/2; 133/3;
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A;Accession: B71689
A;Status: preliminary; nucleic acid sequence not shown; transl
                                                                                                                                                                                                                                                                                                                               hypothetical protein RP328 - Rickettsia prowazekii
C;Species: Rickettsia prowazekii
C;Date: 21-Nov_1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000
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A; Residues: 1-311 <AND>
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Best Local Similarity 100
Matches 13; Conservative
   Query Match
Best Local Similarity
Matches 11; Conserv
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   Conservative
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Pred. No.
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Pred. No.
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Pred. No.
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0.00021
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                                Length 311;
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early protein p12 - phage PRD1
C;Species: phage PRD1
C;Date: 03-Aug-1990 #sequence_revision
C;Accession: A35148; JQ0186
R;Gerendasy, D.; Ito, J.
J. Bacteriol. 172, 1889-1898, 1990
                                                                                                                                                                                                                                                                                                                                         A;Map position: 2
A;Introns: 72/2; 265/2
C;Superfamily: erythrocyte band 7 integral membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              conserved hypothetical protein SPBC16G5.07c - fissi
C;Species: Schizosaccharomyes pombe
C;Date: 03-Dec1999 #sequence_revision 03-Dec-1999
C;Accession: T39599
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R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, Science 293, 2093-2098, 2001

A;Title: Mechanisms of Evolution in Rickettsia conorii al A;Reference number: A97700; MUID:21442074; PMID:11557893

A;Accession: D97756
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D97756
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A; Residues: 1-354 <LYN>
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C; Superfamily:
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A; Residues: 1-312 < KUR>
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C; Date: 30-Sep-2001 #sequence_revision
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100.0%;
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Pred. No. 0.013;
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                                                     03-Aug-1990
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1998
                                                                                                                                                                                                                                                                        DB 2;
0.014;
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                                                       08-Oct-1999
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R.Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: E87425
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:M30146; NID:g215762; PIDN:AAA32453.1; PID:g215763
R;Pakula, T.M.; Savilahti, H.; Bamford, D.H.
Gene 85, 53-58, 1989
A;Title: The organization of the right-end early region of bacteriophage PRD1 genome.
A;Reference number: JQ0186; MUID:90152379
A;Accession: JQ0186; MUID:90152379
A;Moccession: JQ0186
A;Residues: 1-160 <PAK>
A;Cross-references: GB:M33428; NID:g215747; PIDN:AAA32447.1; PID:g215748
C;Keywords: DNA binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein C0800w - malaria parasite (Plasmodium falciparum) C;Species: Plasmodium falciparum C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000 C;Accession: T18493 R;Lawson, D.; Bowman, S.; Barrell, B. submitted to the EMBL Data Library, August 1997 A;Reference number: Z18935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Nucleotide sequence and transcription of the right early region of bacteriophag
A;Reference number: A35148; MUID:90202706
A;Accession: A35148
    A;Molecule type: DNA
A;Residues: 1-248 <STO>
A;Cross-references: GB:AE005673; NID:gl3422783; PIDN:AAK23401.1; GSPDB:GN00148
C;Genetics:
                                                                                                                                                                                                                                                                   transcription regulator, GntR family [imported] - Caulobacter crescentus C;Species: Caulobacter crescentus C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 30-Sep-2001 C;Accession: E87425
                                                                                                                                                                                                                                                                                                                                                               RESULT
E87425
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A;Accession: T18493
A;Status: preliminary; translated
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A; Note: C0800w
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C;Genetics:
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A; Residues: 1-374 <LAW>
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A; Residues: 1-160 <GER>
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Best Local Similarity
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Query Match
Best Local Similarity
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C;Accession: G83163
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, Radman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, Lory, S.; Olson, M.V.
                                                                                                                                                                                                                                                           Curr. Top. Microbiol. Immunol. 154, 125-169, 1990
A;Title: Analysis of the protein-coding content of the sequence of human cytomegalovi A;Reference number: S09749; MUID:90269039
A;Accession: S09777
F;1-25/Domain: signal sequence #status predicted <SIG>F;26-343/Product: hypothetical protein ULI4 #status pref;28-345/Domain: transmembrane #status predicted <TMM>F;160,255/Binding site: carbohydrate (Asn) (covalent) #
                                                                                                                    A;Cross-references: EMBL:X17403; NID:g59591; PIDN:CAA35447.1; PID:g59619 A;Note: this sequence was submitted to the EMBL Data Library, December 1:C;Superfamily: human cytomegalovirus hypothetical protein UL14
                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-343 <CI
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C;Superfamily: pyruvate dehydrogenase complex repressor
                                                                                           C;Superfamily: human cytomegalovirus hypothetical protein
C;Keywords: glycoprotein; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                       R;Chee, M.S.; Bar
M.; Barrell, B.G.
                                                                                                                                                                                                                                                                                                                                                                                                            A;Note: host Homo sapiens (man)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein UL14 precursor - human cytomegalovirus (strain AD169)
C;Species: human cytomegalovirus, human herpesvirus 5
A;Note: host Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:AE004803; GB:AE004091; NID:g9950035; PIDN:AAG07252.1; GSPDB:GNA;Experimental source: strain PAO1
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A; Residues: 1-263 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000
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                                                                                                                                                                                                                                     A; Status: nucleic acid sequence not shown; translation
                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession: S09777
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Experimental source:
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8; Conser
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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; De ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Y.; Liu, Z.A.; Luros, J.S.; Maiti, R.; M.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: C96680
                                                                                                                                                                                                                                                                                                           A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD3252; PMID:11756688
A;Status AG3259
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R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
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                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-400 <KUR>
A;Cross-references: GB:AE008917; PIDN:AAL51242.1; PID:g17981931; GSPDB:GN00190
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A; Residues: 1-398 <STO>
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                                                                                                                                                                     A; Map position: I
                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein BMEI0060 [imported] - Brucella melitensis (strain 16M) C; Species: Brucella melitensis C; Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
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                                                                                                                                                                                                                       A; Experimental source:
                                                                                                                                                                                                                                                                                                   A;Status: preliminary
                                                                      Query Match 2.7
Best Local Similarity 100
Matches 8; Conservative
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Matches 8; Conserv
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R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Gold A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium A;Reference number: A97359; PMID:11743194
                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        aldehyde dehydrogenase dhas [imported] - Agrobacterium tumefaciens (strain C58, Cereo C;Specias: Agrobacterium tumefaciens C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002 C;Accession: D98209
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Best Local Similarity
~+~hes 8; Conserv
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A;Introns: 20/2; 49/2; 113/1; 169/1; 260/2; 375/3;
C;Superfamily: Caenorhabditis elegans hypothetical
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                                                                                                                                                         C; Superfamily: aldehyde
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A; Residues: 1-493 <KUR>
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A; Residues: 1-477 <WIL>
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253 AKAEAIRI 260
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                                                                                                                                                       dehydrogenase (NAD+); aldehyde dehydrogenase
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                                       Score 8; DB 2; Pred. No. 18; 0; Mismatches
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Result
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
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US-09-629-469A-11010
US-10-219-793-411
US-60-389-987-1904
US-60-389-987-7826
US-60-389-987-7826
US-60-389-987-826
US-60-389-987-826
US-10-219-793-418
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US-10-219-793-417
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US-10-219-793-425
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US-09-898-216-1
Sequence 1, Application US/09898216
GENERAL INFORMATION:
Query Match
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US-60-360-039-14424	US-60-360-039-11494	US-10-155-881-10456	US-10-219-999-49786	US-10-203-139-25711	US-10-203-138-10872	US-10-203-137-26806	US-10-203-135-25573	US-10-182-998-10609	US-10-182-997-18957	US-10-182-993-25978	US-10-203-136-26573	US-10-203-134-26567	US-10-182-995-20314	US-10-227-616-59	US-10-179-131-6612	US-10-227-616-58	US-10-219-999-55341	US-10-219-999-39902
Sequence 14424, A	Sequence 11494, A	Sequence 10456, A	Sequence 49786, A	Sequence 25711, A	Sequence 10872, A	Sequence 26806, A	Sequence 25573, A	Sequence 10609, A	Sequence 18957, A	Sequence 25978, A	Sequence 26573, A	Sequence 26567, A	Sequence 20314, A	Sequence 59, Appl	Sequence 6612, Ap	Sequence 58, Appl	Sequence 55341, A	Sequence 39902, A

ALIGNMENTS

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; LIBRARY: Consensus
; CLONE: Consensus
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-898-216-1
                                                                                                                                                                                                                          TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN MEMBRANE PROTEIN
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Versic
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/898,216
FILING DATE: 02-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/781,562
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
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COMPUTER READABLE FORM:
                                                                                                                             LENGTH: 356 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear
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Score 354;

DB 5

Length 356;

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APPLICANT: OTSUKI, TETSUJI
TITLE OF INVENTION: PRIMERS FOR SYNTHESIZING FUI
FILE REFERENCE: 084335/0123
CURRENT APPLICATION UNMBER: US/09/629,469A
CURRENT FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: JP 1999-300253
PRIOR TILING DATE: 1999-07-29
PRIOR APPLICATION NUMBER: JP 2000-118776
PRIOR APPLICATION NUMBER: JP 2000-118776
PRIOR APPLICATION NUMBER: JP 2000-183767
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: JP 2000-241899
PRIOR APPLICATION NUMBER: JP 2000-241899
PRIOR APPLICATION NUMBER: 60/159,590
PRIOR APPLICATION NUMBER: 60/183,322
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                                                                                      SOFTWARE: Patentin Ver. 2
SEQ ID NO 11010
LENGTH: 356
TYPE: PRT
ORGANISM: Homo sapiens
US-09-629-469A-11010
Query Match
Best Local Sim
Matches 318;
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APPLICANT: ISOG
APPLICANT: NISH
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ISHII, SHIZUKO
SUGIYAMA, TOMOYASU
WAKAMATSU, AI
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Score 218; DE
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CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: 09/209,462
PRIOR FILING DATE: 1998-12-11
PRIOR APPLICATION NUMBER: PCT/US98/12125
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/049,547
PRIOR FILING DATE: 1997-06-13
PRIOR APPLICATION NUMBER: 60/049,548
PRIOR APPLICATION NUMBER: 60/049,548
PRIOR APPLICATION NUMBER: 60/049,549
PRIOR FILING DATE: 1997-06-13
PRIOR APPLICATION NUMBER: 60/049,549
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PRIOR APPLICATION NUMBER: 60/049,549
PRIOR FILING DATE: 1997-06-13
                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/049,550
PRIOR FILING DATE: 1997-06-13
PRIOR APPLICATION NUMBER: 60/049,566
PRIOR FILING DATE: 1997-06-13
PRIOR APPLICATION NUMBER: 60/049,606
PRIOR FILING DATE: 1997-06-13
PRIOR APPLICATION NUMBER: 60/049,607
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PRIOR APPLICATION NUMBER: 60/049,607
PRIOR FILING DATE: 1997-06-13
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APPLICANT: Rosen et
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                                                                                                       APPLICATION NUMBER: 60/0
FILING DATE: 1997-06-13
APPLICATION NUMBER: 60/0
FILING DATE: 1997-07-08
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APPLICATION NUMBER: 60/
FILING DATE: 1997-06-13
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                  NUMBER:
                                    1997-09-1
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                                                   60/058,665
                                                                                      60/055,984
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Sequence 411, Application US/10219793
GENERAL INFORMATION:
APPLICANT: ROSen et al.
TITLE OF INVENTION: 86 Human Secreted Proteins
FILE REFERENCE: PZ008P1C1
CURRENT APPLICATION NUMBER: US/10/219,793
CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: 09/209,462
PRIOR APPLICATION NUMBER: PCT/US98/12125
PRIOR FILING DATE: 1998-06-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Homo
US-10-219-793-150
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SEQ ID NO 150
LENGTH: 356
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Best Local Similarity
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FILING DAYE: 1997-10-02
APPLICATION NUMBER: 60/060,865
FILING DAYE: 1997-10-02
APPLICATION NUMBER: 60/061,059
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APPLICATION NUMBER: 60/
FILING DATE: 1997-10-02
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FILING DATE: 1997-10-02
APPLICATION NUMBER: 60/060,841
FILING DATE: 1997-10-02
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Pred. No. 8e-197;
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US-10-219-793-411
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PRIOR APPLICATION NUMBER: 60/660,834
PRIOR FILLING DATE: 1997-10-02
PRIOR APPLICATION NUMBER: 60/060,841
PRIOR FILING DATE: 1997-10-02
PRIOR PRIOR FILING DATE: 1997-10-02
PRIOR FILING DATE: 1997-10-02
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PRIOR APPLICATION NUMBER: 60/058,665
PRIOR FILING DATE: 1997-09-12
PRIOR APPLICATION NUMBER: 60/058,668
PRIOR FILING DATE: 1997-09-12
PRIOR APPLICATION NUMBER: 60/058,669
PRIOR FILING DATE: 1997-09-12
                                                                                SOFTWARE: Pa
SEQ ID NO 411
                                                                                                                          PRIOR FILING DATE: 1997-10-02
NUMBER OF SEQ ID NOS: 737
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PRIOR APPLICATION NUMBER: 60
PRIOR FILING DATE: 1997-09-1
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PRIOR APPLICATION NUMBER: 60
PRIOR FILING DATE: 1997-06-1
PRIOR APPLICATION NUMBER: 60
PRIOR FILING DATE: 1997-06-1
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                                       LENGTH: 306
TYPE: PRT
                 ORGANISM: Homo sapiens
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APPLICATION NUMBER: 60/052,989
FILING DATE: 1997-06-13
APPLICATION NUMBER: 60/051,919
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APPLICATION NUMBER: 60/049,609
FILING DATE: 1997-06-13
APPLICATION NUMBER: 60/049,610
FILING DATE: 1997-06-13
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FILING DATE: 1997-06-13
APPLICATION NUMBER: 60/049,607
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APPLICATION NUMBER: 60/055,984
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Š Best Loc Matches Query Match 144 Local l Similarity 202; Conser 56.7%; Silarity 100.0%; Conservative 0; Score 202; DB; Pred. No. 8.4
0; Mismatches DB 6; Le 8.4e-182; 0 Length 306; 0; Gaps 0;

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; LENGTH: 356
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-389-987-1904
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APPLICANT: Fahy, Eoin D.
APPLICANT: Zhang, Bing
APPLICANT: Gibson, Bradford W
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
APPLICANT: Glenn, Gary M.
APPLICANT: Warnock, Dale E.
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Best Local S
Matches 202
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TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088 465P2
CURRENT APPLICATION NUMBER: US/60/389,987
CURRENT FILING DATE: 2002-06-17
NUMBER OF SEQ ID NOS: 3025
SOFTWARE: F88tSEQ for Windows Version 4.0
SEQ ID NO 1904
                                                                                                                                                                                  Sequence 826, Application US/60389987 GENERAL INFORMATION:
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GENERAL INFORMATION:
                                                                                                          APPLICANT: Ghosh, Soumitra S.
APPLICANT: Fahy, Eoin D.
APPLICANT: Zhang, Bing
APPLICANT: Gibson, Bradford
APPLICANT: Zhang, Bing
APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
APPLICANT: Warrock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088.465P2
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                                                                                                                                                                                                                                                                                            ALTQHNGDAAASLTVAEQYVSAFSKLAKDSNTILLPSNPGDVTSNVAQAMGVYGALTKAP 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VPGTPDSLSSGSSRDVQGTDAS 295
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APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
APPLICANT: Glenn, Gary M.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088.465P2
CURRENT APPLICATION NUMBER: US/60/389,987
CURRENT APPLICATION NUMBER: US/60/389,987
NUMBER OF SEQ ID NOS: 3025
SOFTWARE: FRASTSEQ for Windows Version 4.0
SEQ ID NO 768
LENGTH: 342
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GENERAL INFORMATION
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CURRENT FILING DATE: 2002-06-17
NUMBER OF SEQ ID NOS: 3025
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 826
LENGTH: 357
TYPE: PRT
                                                                                                                                                                                                                                                                                    Query Match
Best Local :
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                                                                                                                                                                                                                                                                Matches 143;
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APPLICANT: Fahy, Eoin D.
                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
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                323 PVPGTPDSLSSGSSRDVQGTDAS 345
                                                                                                         263 AALTQHNGDAAASLTVAEQYVSAFSKLAKDSNTILLPSNPGDVTSMVAQAMGVYGALTKA 322
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309
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                                                                                  AALTQHNGDAAASLTVAEQYVSAFSKLAKDSNTILLPSNPGDVTSMVAQAMGVYGALTKA
PVPGTPDSLSSGSSRDVQGTDAS 331
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100.0%; Pred. No. 3.7e-126;
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RESULT 8 US-10-219-793-416; Sequence 416, A

Application US/10219793

INFORMATION

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: SEQ ID NO 416

: LENGTH: 60

: TYPE: PRT

: ORGANISM: Homo sapiens

US-10-219-793-416
                                                                  NUMBER OF SEQ ID NO SOFTWARE: Patentin
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CURRENT FILING DATE: 2002-08-16
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TITLE OF INVENTION: 86 Human Secreted Proteins
FILE REFERENCE: PZ008P1C1
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FILING DATE: 1997-10-02
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FILING DATE: 1997-06-13
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US-10-219-793-418
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FILING DATE: 1997-09-12
APPLICATION NUMBER: 60/
FILING DATE: 1997-10-02
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FILING DATE: 1997-09-12
APPLICATION NUMBER: 60/058,750
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APPLICATION NUMBER: 60
FILING DATE: 1997-09-1
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APPLICATION NUMBER: 60/051,919
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NUMBER: 60/060,841: 1997-10-02
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                                                                60/058,975
                                                                                             60/058,972
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                                      60/060,834
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9.9e-47;
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PRIOR FILING DATE: 1997-10-02
PRIOR APPLICATION NUMBER: 60/061,060
PRIOR FILING DATE: 1997-10-02
NUMBER OF SEQ ID NOS: 737
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION.

PRIOR FILING DATE: 1997-06-13

PRIOR APPLICATION NUMBER: 60/049,548

PRIOR FILING DATE: 1997-06-13

PRIOR FILING DATE: 1997-06-13
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CURRENT FILING DATE: 2002-08-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Rosen et al. TITLE OF INVENTION: 86 Human Secreted Proteins FILE REFERENCE: PZ008P1C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 1998-06-11
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                                   APPLICATION NUMBER: 60/058,665 FILING DATE: 1997-09-12
                                                                                                              APPLICATION NUMBER: 60/051,919 FILING DATE: 1997-07-08
                                                                                                                                                   APPLICATION NUMBER: 60/052,989 FILING DATE: 1997-06-13
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EILING DATE: 1997-06-13

APPLICATION NUMBER: 60/050,901

FILING DATE: 1997-06-13
                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/049,610 FILING DATE: 1997-06-13
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FILING DATE: 1997-06-13
APPLICATION NUMBER: 60/049,609
FILING DATE: 1997-06-13
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FILING DATE: 1997-06-13
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FILING DATE: 1997-06-13
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APPLICATION NUMBER: 60/060,865
FILING DATE: 1997-10-02
                 APPLICATION NUMBER: 60/058,668
                                                                          FILING DATE: 1997-08-18
                                                                                          APPLICATION NUMBER: 60/055,984
1997-09-12
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RESULT 11
US-10-219-793-422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/219,793
CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: 09/209,462
PRIOR FILING DATE: 1998-12-11
PRIOR APPLICATION NUMBER: PCT/US98/12125
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/049,547
PRIOR FILING DATE: 1997-06-13
PRIOR APPLICATION NUMBER: 60/049,548
PRIOR APPLICATION NUMBER: 60/049,548
PRIOR APPLICATION NUMBER: 60/049,548
PRIOR APPLICATION NUMBER: 60/049,548
PRIOR FILING DATE: 1997-06-13
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PRIOR APPLICATION NUMBER: 60/058,750
PRIOR FILING DATE: 1997-09-12
PRIOR PELICATION NUMBER: 60/058,971
PRIOR PELICATION NUMBER: 60/058,972
PRIOR PELICATION NUMBER: 60/058,972
PRIOR PELICATION NUMBER: 60/058,975
PRIOR PELICATION NUMBER: 60/058,975
PRIOR PELICATION NUMBER: 60/058,975
PRIOR PELICATION NUMBER: 60/060,834
PRIOR FILING DATE: 1997-09-12
PRIOR PELICATION NUMBER: 60/060,841
PRIOR PELICATION NUMBER: 60/060,841
PRIOR APPLICATION NUMBER: 60/060,844
PRIOR APPLICATION NUMBER: 60/060,844
PRIOR FILING DATE: 1997-10-02
PRIOR APPLICATION NUMBER: 60/060,865
PRIOR APPLICATION NUMBER: 60/061,059
PRIOR APPLICATION NUMBER: 60/061,059
PRIOR APPLICATION NUMBER: 60/061,059
PRIOR APPLICATION NUMBER: 60/061,060
PRIOR APPLICATION NUMBER: 60/061,060
PRIOR FILING DATE: 1997-10-02
PRIOR APPLICATION NUMBER: 60/061,060
PRIOR FILING DATE: 1997-10-02
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PRIOR FILING DATE: 1997-06-13
PRIOR APPLICATION NUMBER: 60/049,550
PRIOR FILING DATE: 1997-06-13
PRIOR APPLICATION NUMBER: 60/049,566
PRIOR FILING DATE: 1997-06-13
PRIOR APPLICATION NUMBER: 60/049,606
PRIOR APPLICATION NUMBER: 60/049,606
PRIOR APPLICATION NUMBER: 60/049,606
PRIOR FILING DATE: 1997-06-13
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GENERAL INFORMATION:
APPLICANT: Rosen et a
TITLE OF INVENTION: 8
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SEQ ID NO 420
LENGTH: 50
TYPE: PRT
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Best Local
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PRIOR APPLICATION NUMBER: 60/049,608
PRIOR FILING DATE: 1997-06-13
PRIOR APPLICATION NUMBER: 60/049,609
PRIOR FILING DATE: 1997-06-13
PRIOR FILING DATE: 1997-06-13
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PRIOR APPLICATION NUMBER: 60/049,607
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Local Similarity 100.0%;
hes 50; Conservative (
APPLICATION NUMBER: 60/049,610 FILING DATE: 1997-06-13
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NVENTION: 86 Human Secreted Proteins
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US-10-213-793-424

Sequence 424, Application US/10219793

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
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HILLOF INVENTION:
FILE REFERENCE: PZ008P1C1
CURRENT FILING DATE: 2002-08-16
CURRENT FILING DATE: 2002-08-16
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                                                 PRIOR APPLICATION NUMBER: 09/209,462
PRIOR FILING DATE: 1998-12-11
PRIOR PPLICATION NUMBER: PCT/US98/12125
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/049,547
PRIOR FILING DATE: 1997-06-13
PRIOR APPLICATION NUMBER: 60/049,548
PRIOR FILING DATE: 1997-06-13
PRIOR FILING DATE: 1997-06-13
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Best Local !
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TYPE: PRT
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FILING DATE: 1997-10-02
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APPLICATION NUMBER: 60/060,844
FILING DATE: 1997-10-02
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   APPLICATION NUMBER: 60/049,549 FILING DATE: 1997-06-13 APPLICATION NUMBER: 60/049,550
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FILING DATE: 1997-10-02
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FILING DATE: 1997-09-12
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FILING DATE: 1997-09-12
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FILING DATE: 1997-10-02
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FILING DATE: 1997-06-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.
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llarity 100.0%; Pred. No. 1.4e-34;
Conservative 0; Mismatches 0;
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                                                                    RESULT 13
US-10-219-793-426
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                Sequence 426, Application US/10219793
GENERAL INFORMATION:
APPLICANT: Rosen et al.
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SEQ ID NO 424
APPLICANT: Rosen et al.
TITLE OF INVENTION: 86 Human Secreted Proteins
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TYPE: PRT
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; ORGANISM: Homo sapiens US-10-219-793-424
                                                                           Query Match 12.6%; Score 45; DB Best Local Similarity 100.0%; Pred. No. 1. Matches 45; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR EPILING DATE: 1997-10-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/051,919
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OR APPLICATION NUMBER: 60/0-
OR APPLICATION NUMBER: 60/0-
OR APPLICATION NUMBER: 60/0-
OR FILING DATE: 1997-06-13
OR FILING DATE: 1997-06-13
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APPLICATION NUMBER: 60/058,972
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APPLICATION NUMBER: 60/055,984
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APPLICATION NUMBER: 60/058,665
FILING DATE: 1997-09-12
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TQHNGDAAASLTVAEQYVSAFSKLAKDSNTILLPSNPGDVTSMVA
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; LENGTH: 46
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-219-793-426
                                                                                                     PRIOR APPLICATION NUMBER: 60/061,059
PRIOR FILING DATE: 1997-10-02
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NUMBER OF SEQ ID NOS: 737
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CURRENT APPLICATION NUMBER: US/10/219,793
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EQ ID NO 426
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FILING DATE: 1997-10-02
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RESULT 14
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APPLICANT: Rosen et
TITLE OF INVENTION:
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PRIOR APPLICATION NUMBER: 09/209,462
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OR FILING DATE: 1997-08-18
OR APPLICATION NUMBER: 60/058,665
OR FILING DATE: 1997-09-12
OR APPLICATION NUMBER: 60/058,668
OR FILING DATE: 1997-09-12
OR APPLICATION NUMBER: 60/058,669
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OR APPLICATION NUMBER: 60/058,750
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OR FILING DATE: 1997-09-12
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DR FILING DATE: 1997-06-13

DR APPLICATION NUMBER: 60/052,989

DR APPLICATION NUMBER: 60/051,919

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APPLICATION NUMBER: 60/049,608 FILING DATE: 1997-06-13 APPLICATION NUMBER: 60/049,609 FILING DATE: 1997-06-13
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FILING DATE: 1997-10-02
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86 Human Secreted Proteins
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US-10-219-793-417
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PRIOR FILING DATE: 1997-10-02
NUMBER OF SEQ ID NOS: 737
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 419
LENGTH: 30
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TITLE OF INVENTION: 86 Human Secreted Proteins
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OR FILING DATE: 1997-06-13
OR APPLICATION NUMBER: 60/049,611
OR FILING DATE: 1997-06-13
OR APPLICATION NUMBER: 60/050,901
OR FILING DATE: 1997-06-13
OR APPLICATION NUMBER: 60/052,989
OR APPLICATION NUMBER: 60/052,989
OR FILING DATE: 1997-06-13
OR FILING DATE: 1997-07-08
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FILING DATE: 1997-06-13
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APPLICATION NUMBER: 60/058,669
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FILING DATE: 1997-06-13
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FILING DATE: 1997-08-18
APPLICATION NUMBER: 60/058,665
FILING DATE: 1997-09-12
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PRIOR FILING DATE: 1997-09-12
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PRIOR FILING DATE: 1997-09-12
PRIOR FILING DATE: 1997-09-12
PRIOR FILING DATE: 1997-10-02
PRIOR APPLICATION NUMBER: 60/060,834
PRIOR FILING DATE: 1997-10-02
PRIOR FILING DATE: 1997-10-02
PRIOR PPLICATION NUMBER: 60/060,844
PRIOR FILING DATE: 1997-10-02
PRIOR APPLICATION NUMBER: 60/060,865
PRIOR APPLICATION NUMBER: 60/060,865
PRIOR APPLICATION NUMBER: 60/061,059
PRIOR APPLICATION NUMBER: 60/061,059
PRIOR FILING DATE: 1997-10-02
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SEQ ID NO 417
LENGTH: 28
TYPE: PRT
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Best Local Similarity 100.0%;
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Search completed: September 22, 2002, 18:35:49 Job time: 296 sec

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Sequence 36, Appl Sequence 37, Appl Sequence 272, App Sequence 411, App Sequence 416, App Sequence 418, App Sequence 420, App Sequence 411, App Sequence 417, App Sequence 273, App Sequence 273, App Sequence 274, App Sequence 273, App Sequence 274, App Sequence 275, App Sequence 417, App Sequence 275, App Sequence 427, App Sequence 428, App Sequence 5413, Ap Sequence 5414, App Sequence 5415, App Sequence 5414

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RESULT 2
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; GENERAL INFORMATION:
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PRIOR FILING DATE: 1998-06-11
PRIOR FILING DATE: 1997-06-13
PRIOR FILING DATE: 1997-06-13
PRIOR APPLICATION NUMBER: 60/049,548
PRIOR APPLICATION NUMBER: 60/049,549
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PRIOR FILING DATE: 1997-06-13
PRIOR APPLICATION NUMBER: 60/049,550
PRIOR APPLICATION NUMBER: 60/049,566
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PRIOR APPLICATION NUMBER: 60/049,606
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TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 14
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LENGTH: 356 amino acid:
TYPE: amino acid
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PRIOR FILING DATE: 1997-10-02
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TYPE: PRT
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FILING DATE: 1997-09-12
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CURRENT APPLICATION NUMBER: PCT/US01/03800A
CURRENT FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 2700
SOFTWARE: CUSTOM
SEQ ID NO 2351
LENGTH: 378
                                                                                                                                                                                                                                                                                                          PCT-US01-04098A-3196; Sequence 3196, Application PC/TUS0104098A; Sequence 3196, Application PC/TUS0104098A; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides; FILE REFERENCE: 21272-029
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                                                      PRIOR APPLICATION NUMBER: 09/728,422
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: 09/693,325
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 09/663,561
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 09/654,936
PRIOR FILING DATE: 2000-09-01
PRIOR FILING DATE: 2000-09-01
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Best Local Similarity
Matches 318; Conserv
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                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: Not Yet Assigned PRIOR FILING DATE: 2001-01-30
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APPLICANT: Tang, Y, Tom et al
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-030
                                         PRIOR
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FILING DATE: APPLICATION
                   APPLICATION NUMBER: 09/620,325 FILING DATE: 2000-07-19
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Pred. No. 4.9e-207;
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; ORGANISM: Homo sapiens PCT-US01-04942A-222
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Best Local Sim
Matches 318;
                                                     SEQ ID NO 222
LENGTH: 3007
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                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: PCT/US01/04942A
CURRENT FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: 09/693,267
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 09/665,363
PRIOR FILING DATE: 2000-09-19
PRIOR PILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-14
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PRIOR APPLICATION NUMBER: 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR FILING DATE: 2000-02-03
                                                                                                         PRIOR APPLICATION NUMBER: 09/574,454
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: 09/519,705
PRIOR FILING DATE: 2000-03-07
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                                      TYPE: PRT
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Pred. No. 4.9e-207;
0; Mismatches 1;
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GENERAL INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: PCT/USO1/08656
CURRENT FILING DATE: 2001-04-16
PRIOR APPLICATION NUMBER: 09/522,929
PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: 09/770,160
PRIOR FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 10994
SOFTWARE: CUStom
                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC FILE REFERENCE: 21272-066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Hyseq, Inc
                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: (1)...(3019)
OTHER INFORMATION: Xaa = X or * as
                                                                                                                                                           -US01-08656-10594
                                                                                                                                                                                                            NAME/KEY: DOMAIN
LOCATION: (2426)..(2903)
OTHER INFORMATION: identified by PFam, accession name AAA, E-value=3.3e-182, PFam
OTHER INFORMATION: score of 618.7
                                                                                                                                                                                                                                                                             NAME/KEY: DOMAIN
LOCATION: (115).. (144)
OTHER INFORMATION: Band 7 protein family proteins domain identified by eMATRIX,
OTHER INFORMATION: accession number BL01270C, p-value=6.745e-17, raw score of 16.91
                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                      ) ID NO 10594
LENGTH: 3019
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                                                                                                        Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PEQSAVTLDNVTLQIDGVLYLRIMDPYKASYGVEDPEYAVTQLAQTTMRSELGKLSXDKV 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TPDSLSSGSSRDVQGTDAS 345
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                                      RASSGLPRNTVVLFVPQQEAWVVERMGRFHRILEPGLNILIPVLDRIRYVQSLKEIVINV 86
PEQSAVTLDNVTLQIDGVLYLRIMDPYKASYGVEDPEYAVTQLAQTTMRSELGKLSXDKV 146
                                                                                             318;
                                                                                            Conservative
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0; Mismatches 1;
                                                                                            0;
                                                                                          Score 218; DB 1;
Pred. No. 3.8e-206;
0; Mismatches 1;
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                                                                                                                    Length 3019;
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; ORGANISM: Homo sapiens 
'US-09-298-733-36
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CURRENT FILING DATE: 1999-04-23
EARLIER APPLICATION NUMBER: 60/082,961
EARLIER FILING DATE: 1998-04-24
EARLIER APPLICATION NUMBER: 60/086,402
EARLIER FILING DATE: 1998-05-22
EARLIER APPLICATION NUMBER: 60/088,'994
EARLIER APPLICATION NUMBER: 60/089,163
EARLIER APPLICATION NUMBER: 60/089,163
EARLIER APPLICATION NUMBER: 60/089,163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Valenzuela, Dario APPLICANT: Yuan, Olive APPLICANT: Hoffman, Heidi APPLICANT: Hall, Jeff APPLICANT: Rapiejko, Peter APPLICANT: Adams, R. Mark APPLICANT: Agostino, Michael JAPPLICANT: Fechtel, Kim APPLICANT: Howes, Steve H.
                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 79
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 36
LENGTH: 305
TYPE: PRT
                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 202; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Secreted Prote TITLE OF INVENTION: Encoding Them FILE REFERENCE: AGI99-02pM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EARLIER APPLICATION NUMBER: 60/091,619 EARLIER FILING DATE: 1998-07-02
                                                                                                                                   204 VLESEGTRESAINVAEGKKQAQILASEAEKAEQINQAAGEASAVLAKAKAKAEAIRILAA 263
                                                                                                                                                                                                              144 DKVFRERESLNASIVDAINQAADCWGIRCLRYEIKDIHVPPRVKESMQMQVEAERRKRAT 203
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                                  PEQSAVTLDNVTLQIDGVLYLRIMDPYKASYGVEDPEYAVTQLAQTTMRSELGKLSLDKV
VPGTPDSLSSGSSRDVQGTDAS
                                                                                                                 VLESEGTRESAINVAEGKKQAQILASEAEKAEQINQAAGEASAVLAKAKAKAEAIRILAA
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345
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                                                                                                                                                                                                                                                                                                           Length 305;
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273 VPGTPDSLSSGSSRDVQGTDAS 294

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; SOFTWARE: FASTSEQ for W:
SEQ ID NO 36
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-298-733A-36
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                                                                                                                                                                                                                                          Sequence 36, Application US/09723594 GENERAL INFORMATION:
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Best Local Similarity
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APPLICANT:
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APPLICANT:
APPLICANT:
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TITLE OF INVENTION: Secreted Proteins and Polynucleotides
TITLE OF INVENTION: Secreted Proteins and Polynucleotides
TITLE OF INVENTION: Secreted Proteins
FILE REFERENCE: 1966.1009-000
CURRENT FILLING DATE: 1996-04-23
CURRENT FILLING DATE: 1999-04-23
PRIOR APPLICATION NUMBER: 60/082,961
PRIOR FILING DATE: 1998-04-24
PRIOR FILING DATE: 1998-04-24
PRIOR APPLICATION NUMBER: 60/086,402
PRIOR APPLICATION NUMBER: 60/088,994
PRIOR APPLICATION NUMBER: 60/088,994
APPLICANT: Raplejko, Peter
TITLE OF INVENTION: Secreted Proteins and Polynucleotides
TITLE OF INVENTION: Encoding Them
FILE REFERENCE: 1966.1009-002
CURRENT FILLORIANTE: 2000-11-28
CURRENT FILLING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 09/298,733
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PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1998-07-02
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               144 DKVFRERESLNASIVDAINQAADCWGIRCLRYEIKDIHVPPRVKESMQMQVEAERRKRAT 203
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Hall, Jeff
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Yuan, Olive
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; SOFTWARE: FastSEQ for Wi
; SEQ ID NO 36
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-723-594-36
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                                        SOFTWARE: Fas
SOFTWARE: Fas
SEQ ID NO 36
FRAGTH: 305
                                                                                                                                                                          FILE REFERENCE: 1966.1009-001

CURRENT APPLICATION NUMBER: US/09/724,497

CURRENT FILING DATE: 2000-11-28

PRIOR APPLICATION NUMBER: 09/298,733

PRIOR FILING DATE: 1999-04-23

PRIOR APPLICATION NUMBER: 60/082,961

PRIOR FILING DATE: 1998-04-24

PRIOR FILING DATE: 1998-04-24

PRIOR APPLICATION NUMBER: 60/086,402

PRIOR APPLICATION NUMBER: 60/086,402

PRIOR FILING DATE: 1998-05-22

PRIOR APPLICATION NUMBER: 60/088,994

PRIOR APPLICATION NUMBER: 60/089,944

PRIOR APPLICATION NUMBER: 60/089,944

PRIOR APPLICATION NUMBER: 60/089,944

PRIOR APPLICATION NUMBER: 60/089,945

PRIOR APPLICATION NUMBER: 60/089,163

PRIOR FILING DATE: 1998-06-01

PRIOR APPLICATION NUMBER: 60/089,163

PRIOR FILING DATE: 1998-66-12
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Best Local Similarity
Matches 202; Conserv
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APPLICANT:
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PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1998-07-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Rapiejko, Peter
TITLE OF INVENTION: Secreted
TITLE OF INVENTION: Encoding
FILE REFERENCE: 1966.1009-001
                                                                                                          NUMBER OF SEQ ID NOS:
                                                                                                                                    PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1998-
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                       LENGTH: 30
TYPE: PRT
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   144 DKVFRERESLNASIVDAINQAADCWGIRCLRYEIKDIHVPPRVKESMOMQVEAERRKRAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     324 VPGTPDSLSSGSSRDVQGTDAS 345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 153 VLESEGTRESAINVAEGKKQAQILASEAEKAEQINQAAGEASAVLAKAKAKAEAIRILAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         204 VLESEGTRESAINVAEGKKQAQILASEAEKAEQINQAAGEASAVLAKAKAKAEAIRILAA 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93 DKVFRERESLNASIVDAINQAADCWGIRCLRYEIKDIHVPPRVKESMQMQVEAERRKRAT 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALTQHNGDAAASLTVAEQYVSAFSKLAKDSNTILLPSNPGDVTSMVAQAMGVYGALTKAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VPGTPDSLSSGSSRDVQGTDAS 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Valenzuela, Dario B.
Yuan, Olive
Hoffmann, Heidi
Hall, Jeff
                                                                                            FastSEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FastSEQ for Windows Version 3.0
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                                                                                            for Windows Version 3.0
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PCT-US98-12125-272
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                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PETELECOMMUNICATION INFORMATION
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
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ADDRESSEE: Human
STREET: 9410 Key
CITY: Rockville
STATE: Maryland
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9410 Key West Avenue
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100.0%; Pr
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                                                                                                              Score 202; DB 1; L, Pred. No. 3e-191; C, Pred. No. 
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; Pred. No. 3e-191;
0; Mismatches 0
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PRIOR FILING DATE: 1997-06-13
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                          FILING DATE: 1997-APPLICATION NUMBER:
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FILING DATE: 1997-09-12
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NUMBER:
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; LENGTH: 358
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-04098A-1228
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                                                                    NUMBER OF SEQ ID NOS: 3960
SOFTWARE: Custom
SEQ ID NO 1228
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Best Local Similarity
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SEQ ID NO 411
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TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-029
                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: Not Yet Assigned PRIOR FILING DATE: 2001-01-30 PRIOR APPLICATION NUMBER: 09/728,422 PRIOR FILING DATE: 2000-11-30 PRIOR FILING DATE: 2000-11-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: PCT/US01/04098A CURRENT FILING DATE: 2001-02-05
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                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 09/663,561
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FILING DATE: 2000-10-20
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APPLICATION NUMBER: 60/
FILING DATE: 1997-10-02
                                                                                                                                                            APPLICATION NUMBER: 09/560,875 FILING DATE: 2000-04-27
                                                                                                                                                                                             APPLICATION NUMBER: 09/598,075 FILING DATE: 2000-06-20
                                                                                                                                                                                                                                                    APPLICATION NUMBER: 09/620,325
                                                                                                                                                                                                                                                                                                        FILING DATE: 2000-09-15
                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                     FILING DATE: 2000-07-19
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; Pred. No. 3e-191;
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PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/04
PRIOR FILING DATE: 1997-06-13
PRIOR APPLICATION NUMBER: 60/04
PRIOR FILING DATE: 1997-06-13
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                               PRIOR APPLICATION NUMBER: 60/058,668 PRIOR FILING DATE: 1997-09-12
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PRIOR FILING DATE: 1997-06-13
PRIOR APPLICATION NUMBER: 60/
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PRIOR FILING DATE: 1997-0
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PRIOR FILING DATE: 1997-06-13
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PRIOR FILING DATE:
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PRIOR APPLICATION NUMBER:
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                                                                  APPLICATION NUMBER: 60/
FILING DATE: 1997-09-12
APPLICATION NUMBER: 60/
FILING DATE: 1997-09-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QHNGDAAASLTVAEQYVSAFSKLAKDSNTILLPSNPGDVTSMVAQAMGVYGALTKAPVP
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99.7%;
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Pred. No. 3.3e-187;
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; LENGTH: 60
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-209-462B-416
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PRIOR FILING DATE: 1997-09-12
PRIOR APPLICATION NUMBER: 60/06
PRIOR APPLICATION NUMBER: 60/06
PRIOR FILING DATE: 1997-10-02
PRIOR APPLICATION NUMBER: 60/06
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PRIOR APPLICATION NUMBER: 60/06
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PRIOR APPLICATION NUMBER: 60/0
PRIOR FILING DATE: 1997-10-02
NUMBER OF SEQ ID NOS: 737
COETHANDE: 747
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CURRENT FILING DATE: 1998-12-11
PRIOR APPLICATION NUMBER: PCT/US98/12125
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PRIOR APPLICATION NUMBER: 60/C
PRIOR FILING DATE: 1997-06-13
PRIOR APPLICATION NUMBER: 60/C
PRIOR FILING DATE: 1997-06-13
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                                  R FILING DATE: 1997-06-13
R APPLICATION NUMBER: 60/04
R FILING DATE: 1997-06-13
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PRIOR APPLICATION NUMBER: 60/060
PRIOR APPLICATION NUMBER: 60/060
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SOFTWARE: PatentIn V
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                                                        16.3%; Score 58; ilarity 100.0%; Pred. No. Conservative 0; Mismatc
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Search completed: September 22, 2002, 18:34:49 Job time: 252 sec

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1: /cgn2_6/ptodata/1.

2: /cgn2_6/ptodata/1.

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/cgn2_6/ptodata/1/iaa/BCTUS_COMB.pep:*
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   US-08-781-562-1
US-08-346-849-32
US-08-293-284A-25
US-08-293-208A-32
US-08-93-008A-4
US-08-152-488-3
US-08-677-304-3
US-08-677-304-3
US-08-93-008A-6
US-08-993-008A-6
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            Sequence 4, Appli
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Query Match
Best Local Similarity
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Sequence 2, Appli	Sequence 11, Appl	Sequence 5, Appli	Sequence 2, Appli	Sequence 5, Appli	Sequence 2, Appli	Sequence 1, Appli	Sequence 2, Appli										

ALIGNMENTS

## Sequence 1, Application US/08781562 Patent No. 5763589 GENERAL INFORMATION: ATTORNEY/AGENT INFORMATION: NAME: Bilings, Lucy J. REGISTRATION UNMBER: 36,749 REFERENCE/DOCKET NUMBER: PF-C TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555 TELEFAX: 415-845-4166 INFORMATION FOR SEQ ID NO: ZIP: 94304 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette SEQUENCE CHARACTERISTICS: LENGTH: 356 amino acids TYPE: amino acid COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA: IMMEDIATE SOURCE: APPLICATION NUMBER: US FILING DATE: Herewith CLASSIFICATION: 530 PRIOR APPLICATION DATA: APPLICANT: Hillman, Jennifer L. APPLICANT: GOII, SUTYA K. TITLE OF INVENTION: NOVEL HUMAN MEMBRANE PROTEIN NUMBER OF SEQUENCES: 7 CORRESPONDENCE ADDRESS: LIBRARY: Consensus CITY: Palo Alto STATE: CA COUNTRY: USA APPLICATION NUMBER: FILING DATE: TOPOLOGY: STRANDEDNESS: ADDRESSEE: Incyte Pharmaceuticals, Inc STREET: 3174 Porter Drive Consensus linear single US/08/781,562 PF-0181 US

99.4%;

Score 354; Pred. No.

0; Bd

Length 356;

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RESULT 2
US-08-346-849-25
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US-08-346-849-25
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Patent No. 5
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APPLICANT: Zhang, Shuguang
APPLICANT: Lockshin, Curtis
                                                                                                TELEFAX: (617) 861-9540 INFORMATION FOR SEQ ID NO: 25:
                                                                                                                                                                                                                                                                                        TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/346,849
FILING DATE:
CLASSIET.
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APPLICANT: LOCKShin, Curtis
APPLICANT: Holmes, Todd
TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
               TOPOLOGY:
                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,326
ETLING DATE: 28 DECEMBER 1992
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRAFION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: MIT-6008
                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
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CITY: Lexington
STATE: Massachus
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                                             amino acid
                 TYPE:
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                                                                                                                                                                                                 TELEPAX: (61/) ... 3:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
FRIGTH: 16 amino acids
                                                                  Query Match
Best Local S
Matches 7
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Best Local S
Matches 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/346,849
251 AKAKAEA 257
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1 AKAKAEA 7
                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 07/973,326
FILING DATE: 28 DECEMBER 1992
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: MIT-6008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Holmes, Todd
TITLE OF INVENTION: STAI
TITLE OF INVENTION: SELI
TITLE OF INVENTION: THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Zhang, Shuguang
APPLICANT: Lockshin, Curtis
APPLICANT: Rich, Alexander
APPLICANT: Holmes, Todd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           249 AKAKAKA 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: Two Militia | CITY: Lexington STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A. ZIP: 02173-4799
                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                TELEPHONE:
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                                                                  Similarity 7; Conserv
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                                                                                                                                                                                              amino acid
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                                                                    Conservative
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                                                                                                                                                                 peptide
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, 100.0%; Pr
                                                                                 2.0%;
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                                                                                 Score 7; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 7; DB 1; Pred. No. 5.8;
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                                                                    Mismatches
                                                                                 DB 1;
                                                                                                Length 16;
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RESULT 4 US-08-293-284A-25

Sequence 25, Application US/08293284A Patent No. 5955343 GENERAL INFORMATION:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local :
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                                                                                                                                                                                                                                                                              Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 22-AUG-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,326

FILING DATE: 28-DEC-1992

ATTORNEY/AGENT INFORMATION:
NAME: BIOOK, DAVId E.
REGISTRATION NUMBER: 22,592

REFERENCE/DOCKET NUMBER: MIT-600

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
                                                                                      APPLICANT: Zhang, Shuguang
APPLICANT: Rich, Alexander
APPLICANT: DiPersio, C. Michael
APPLICANT: Lockshin, Curtis
TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY
TITLE OF INVENTION: STERFOR
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOM
STREET: Two Militia Drive
                                                                                                                                                                                                                        APPLICANT:
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ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTITIES AND USES TITLE OF INVENTION: THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
nes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Lexington
STATE: Massachus
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                     CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                                                            2 AKAKAKA 8
                                                                                                                                                                                                                                                            INFORMATION:
                                                                                                                                                                                                                                                                                2, Application US/08293284A
5955343
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Massachusetts
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DiPersio, C. Michael
Lockshin, Curtis
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                                                                                                                                                                                                                                         Holmes, Todd
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                                                    BROOK, SMITH & REYNOLDS, P.C
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Best Local S
Matches 7
               COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-POS
SOFTWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,008A
FILING DATE: 18-DEC-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/032,436
FILING DATE: 18-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sullivan, Sally A.
REGISTRATION NUMBER: 32,064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08993008A Patent No. 6153596 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 22-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,326
FILING DATE: 28-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: MIT-6008A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                      COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan
STREET: 5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Relicurrent APPLICATION DATA: APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Liotta, Dennis C
                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          251 AKAKAEA 257
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CITY: Boulder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                   STATE:
REFERENCE/DOCKET NUMBER:
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Karr, Joan F.
Pohl, Jan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (617) 861-9540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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Query Match
Best Local Similarity
Thes 7; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                           TELEFAX: 908-276-5543
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Benita J, Rohm, Esq.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: pe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
ORGANISM: N/A
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE:
                                MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
                                                                                                                                                                          TELECOMMUNICATION INFORMATION: 908-276-3344
                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/
FILING DATE: 14-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: WordPerfect CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 303-499-8080
                                                                                                                                                                                                                                     NAME: Rohm, Benita J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           249 AKAKAKA 255
                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/152,488 FILING DATE: 12-NOV-1993 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 512 Spring
CITY: Cranford
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 24 amino acids
TYPE: amino acid
TYPE: amino acid
STRANDEDNESS: not rele
                                                                                                                                                                                                         REGISTRATION NUMBER: 28, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                              STRANDEDNESS:
                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 AKAKAKA 8
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                                                                                              amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        512 Springfield Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 303-499-8089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stanley, James C.
VENTION: NOVEL PEPTIDES FOR HEPARIN AND
VENTION: LOW MOLECULAR WEIGHT HEPARIN
VENTION: ANTICOAGULATION REVERSAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                              N/A
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100.0%; Pred. No.
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                      PCT/US92/08069
                                                                                                                                                                                                                        28,664
                                                                                                                                                                                                                                                                                                                                                                                6; ASCII (DOS) Text
                                                                                                                                                                                                            RM-7WG
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; DOCUMENT NUMBER: PCT/US92/08069
; FILING DATE: 14-AUG-1993
US-08-152-488-3
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Best Local Similarity
Trahas 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                     TELEFAX: 313-496-8454
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE: N/A
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US92/06829
FILING DATE: 14-AUG-1992
APPLICATION NUMBER: US 08/152,488
FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: ROhm, Benita J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy diskette 3.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: MS-DOS v.6.22
SOFTWARE: WordPerfect 6.1; ASCII (DOS)Text
CURRENT APPLICATION DATA:
                                                                  PUBLICATION INFORMATION
                                                                                                  MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/303,025 FILING DATE: 08-SEPT-1994 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Michig
                                                                                                                                                                                                                                                                                        NAME: Rohm, Benita J. REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 48226-4415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
DOCUMENT NUMBER: PCT/US92/08069 FILING DATE: 14-AUG-1993
                                                                                    ORGANISM:
                                                                                                                                  TOPOLOGY:
                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                     TELEPHONE:
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                                                   AUTHORS:
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                                     N/A
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150 West Jefferson, Suite 2500
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VENTION: NOVEL PEPTIDES FOR HEPARIN AND
VENTION: LOW MOLECULAR WEIGHT HEPARIN
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                                                                                                                                  N/A
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                                                                                                                    peptide
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Pred. No.
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Query Match

2.0%; Score 7;

DB 1;

Length

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PUBLICATION INFORMATION:

PUBLICATION INFORMATION:

DOCUMENT NUMBER: PCT/US92/08069

FILING DATE: 14-AUG-1993

US-08-677-304-3
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Best Local Similarity luu.
Thes 7; Conservative
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                                                                                                                                                                                                                                                                                                                                            TELEFAX: 908-276-5543
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Stanley, TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6; ASCII (DOS)Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: RM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-276-3344
                                                                                                                                                                                                                                                       MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                           PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
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                            249 AKAKAKA 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 512 Sp
CITY: Cranford
                                                                                                                                                                                                                                                                                       STRANDEDNESS:
TOPOLOGY: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                            ORGANISM: N/A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 530
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4 AKAKAKA 10
                                                                                                                                                                                                                                                                                                                 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Benita J, Rohm, Esq. 512 Springfield Avenue
                                                                                                                                                                                                                                                                                                                                 29 amino acids
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IVENTION: NOVEL PEPTIDES FOR HEPARIN AND IVENTION: LOW MOLECULAR WEIGHT HEPARIN
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No. 5721212 Relevant
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                                                                      Score 7;
Pred. No.
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                                                                                    Length 29;
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RESULT 10
US-08-436-703B-8
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US-08-436-703B-8
                                                            Best Loc
Matches
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                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION: APPLICANT: Wakefi
                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                   MOLECULE TYPE: peptide ORIGINAL SOURCE: ORGANISM: N/A PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: WORDPERFECT (SOFTWARE: ASCII (DOS)TACURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: N/A FILING DATE: N/A ATTORNEY/AGENT INFORMATION: NAME: Rohm, Benita J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 313-965-1976
                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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                               249 AKAKAKA 255
                                                              Local Similarity hes 7; Conserv
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REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 08-MAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 6601 Woodward Avenue
STREET: Suite 1525
                                                                                                                                                                                                                                                                LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS: N/A
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4 AKAKAKA 10
                                                                                                                                                                                                                                                  TOPOLOGY: N/A
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7: United States of America
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                                                              Conservative
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ASCII (DOS)Text
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Benita J.
...Benita J.
...arwaeR: 28,664
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08-MAY-1995
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100.0%; Fi
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                                                          %; Score 7; DB 2
%; Pred. No. 9.8
0; Mismatches
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                                                                           DB 2;
                                                                                         Length 29;
                                                              Indels
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                                                            Gaps
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US-08-995-172-18; Sequence 18, Application US/08995172B; Patent No. 6218112; GENERAL INFORMATION:

APPLICANT: Thatcher, David R

RESULT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 18
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/08/995,172B
CURRENT FILING DATE: 1997-12-22
EARLIER APPLICATION NUMBER: 60/033,908
EARLIER FILING DATE: 1996-12-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: OPt1 FILE REFERENCE: CACO0026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wilks, Paula
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: UNSURE
LOCATION: (35)
OTHER INFORMATION: Xaa is Cys with Acm sidechain
                                TELEFAX: 303-499-8089 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Polycationic Oligomers
UNMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan
STREET: 5370 Manhattan Circle, Suite 201
                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60
FILING DATE: 18-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 303-499-8080
                SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 18-DEC CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Boulder
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                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                      REGISTRATION NUMBER:
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                                                                 TELEPHONE:
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48 amino acids
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Petros, John A.
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Pohl, Jan
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                                                                                                                                                                                                                                      UMBER: US/08/993,008A
18-DEC-1997
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100.0%; Pr
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Pred. No.
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Query Match
Best Local Similarity
Matches 7; Conser
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INFORMATION FOR SEQ
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HYPOTHETICAL: N
ANTI-SENSE: NO
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APPLICANT:
APPLICANT:
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MEDIUM TYPE: Floppy disk
                                                                                        MOLECULE TYPE: PORTHETICAL: NO
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ATTORNEY/AGENT INFORMATION:
NAME: Sullivan, Sally A.
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                               ANTI-SENSE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                               TYPE: amino acid
STRANDEDNESS: no
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                                                                                                                                                        LENGTH:
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Karr, Joan F.
Pohl, Jan
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             Score 7; I
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US-08-769-211-2
; Sequence 2, Application US/08769211
; Patent No. 5830852
; Patent No. 5830852

GENERAL INFORMATION:

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LENGTH: 60 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-769-211-2
                                                                                                                                                                                                                                                                                                                                                                                     В
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                                                                                                                                                                                                                                                  Sequence 6, Application US/08995172B Patent No. 6218112
SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 6
                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                   APPLICANT: Thatcher, David R
APPLICANT: Wilks, Paula E
TITLE OF INVENTION: Optimization of Gene Delivery and Gene Delivery Systems
FILE REFERENCE: CACCO026
CURRENT APPLICATION NUMBER: US/08/995,172B
CURRENT FILING DAYE: 1997-12-22
EARLIER APPLICATION NUMBER: 60/033,908
EARLIER FILING DAYE: 1996-12-23
NUMBER OF SEQ ID NOS: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Kathleen M. Williams
REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: 3255/02514
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-345-9110
TELEPAX: 617-345-9111
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/769,211
FILING DATE: 18-Dec-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 6.1
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Inc.
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TITLE OF INVENTION: Improved Pharmaceutical Compositions
TITLE OF INVENTION: Insulin-Receptor Mediated Gene Therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
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STATE: Massa
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; OTHER INFORMATION: Description of Artificial Sequence: Peptide US-08-995-172-6
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                                            Query Match
Best Local Similarity
Matches 7; Conser
                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                     LENGTH: 61
                      249 AKAKAKA 255
24 AKAKAKA 30
                                               Conservative
                                                          2.0%;
                                            0;
                                                        Score 7; DB 4;
Pred. No. 19;
                                               Mismatches
                                               0;
                                                                    Length 61;
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Search completed: September 22, 2002, 18:32:15 Job time: 343 sec

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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*

2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

6: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

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US-60-389-987-978-8
US-60-389-987-98-6
US-10-219-999-39902
US-10-219-999-5341
US-10-219-999-5341
US-10-219-999-516-9
US-09-898-216-778-140
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US-09-791-537-98761
US-09-698-180-2
US-09-898-216-7
US-09-898-216-7
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Sequence 1, Appli
Sequence 11010, Ap
Sequence 150, App
Sequence 788, App
Sequence 826, App
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Sequence 98751, A
Sequence 98751, Ap
Sequence 75409, A
Sequence 7409, A
Sequence 7, Appli
Sequence 7, Appli
Sequence 418, App
Sequence 418, App
Sequence 338, App
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RESULT 1  US-09-898-216-1  US-09-898-216.  Sequence 1, Application US/09898216  GENERAL INFORMATION:  APPLICANT: Hillman, Jennifer L.  GOII, SUTYA K.  TITLE OF INVENTION: NOVEL HUMAN MEMBRANE PROTEIN  NUMBER OF SEQUENCES: 7  CORRESSEE: INCYTE PHARMACEULICALS, Inc.  STREET: 3174 PORTER DAY  COUNTRY: USA  ZIP: 94304  COUNTRY: USA  ZIP: 94304  COUNTRY: USA  ZIP: 94304  COMPUTER READABLE FORM:  MEDIUM TYPE: DIS Mette  COMPUTER READABLE FORM:  MEDIUM TYPE: DIS Mette  COMPUTER: FRATION SYSTEM: DOS  SOFTWARE: FRATION DOS  SOFTWARE: FRATION DAY  APPLICATION NUMBER: US/99/898,216  FILING DATE: 02-JU1-2001  CLASSIFICATION NUMBER: US/99/898,216  FILING DATE: 02-JU1-2001  RESISTRATION NUMBER: 08/781,562  FILING DATE: 02-JU1-2001  RESISTRATION NUMBER: 08/781,562  FILING DATE: 415-85-0555  TELEFAX: 415-85-0555  TELEFAX: 415-85-0555  TELEFAX: 415-85-0555  TELEFAX: 415-85-0555  INFORMATION FOR SEQ ID NO: 1:  SEQUENCE CHARACTERISTICS:  LENGTH: 356 amino acid  STYPE: AND ACIDENT SEQ ID NO: 1:  LIBRARY: CONSENSUS  SEQUENCE CHARACTERISTICS:  LIBRARY: CONSENSUS  SEQUENCE DESCRIPTION: SEQ ID NO: 1:	· ALIGNMENTS	27 281.5 15.9 288 6 US-10-223-088-338 28 281.5 15.9 288 6 US-10-223-000-338 28 281.5 15.9 288 6 US-10-223-000-338 29 271 15.3 280 5 US-09-898-216-4 30 263.5 14.9 34.7 1 PCT-USO2-13142-3455 31 263.5 14.9 50 6 US-10-219-793-420 32 261 14.8 50 6 US-10-219-793-425 33 256.5 14.5 34.7 1 PCT-USO2-13142-8455 34 256.5 14.5 34.7 1 PCT-USO2-13142-8455 35 255.5 14.5 35.9 6 US-10-129-713-426 255.5 14.5 35.9 6 US-10-219-793-415 37 224 12.7 46 6 US-10-219-793-426 38 221 13.1 70 6 US-10-219-793-426 38 221 12.7 45 6 US-10-219-793-424 39 211 11.9 45.6 US-10-219-793-424 40 209.5 11.9 38.3 US-10-219-793-424 41 11.5 10.3 38.6 US-10-155-881-30739 42 182.5 10.3 33.6 6 US-10-219-999-57141 43 172.5 9.8 32.9 6 US-10-219-999-57280 45 170.5 9.6 284 6 US-10-219-999-57280
		Sequence 338, App sequence 4, Appli sequence 3455, Ap sequence 420, App Sequence 4455, Ap sequence 415, Ap sequence 415, Ap sequence 424, App sequence 424, App sequence 424, App sequence 833, App sequence 53682, A sequence 57141, A sequence 57280, A sequence 57280, A

Query Match

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Score 1763;

DB 5;

Length 356;

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PRIOR FILING DATE: 1999-07-29
PRIOR APPLICATION NUMBER: JP 1999-300253
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: JP 2000-118776
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: JP 2000-183767
PRIOR FILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-05-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION
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APPLICANT: ISOG
APPLICANT: NISH
APPLICANT: HAYA
APPLICANT: SAIT
APPLICANT: YAMA
 Best Local Sigmatches 341;
               Query Match
Best Local
                                                                                                                 SEQ ID NO 11010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 11010, Application US/09629469A
                                                             LENGTH: 356
TYPE: PRT
ORGANISM: Homo sapiens
-09-629-469A-11010
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                               APPLICANT: OTSUKI, TETSUJI
TITLE OF INVENTION: PRIMERS FOR SYNTHESIZING
FILE REFERENCE: 084335/0123
                                                                                                                                         PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 2000-03 NUMBER OF SEQ ID NOS: 1903
                                                                                                                              SOFTWARE: PatentIn
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nes 356; Conserva
                                                                                                                                                                               APPLICATION NUMBER: JP 2000-241899
FILING DATE: 2000-06-09
APPLICATION NUMBER: 60/159,590
FILING DATE: 1999-10-18
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                                                                                                                                          SEQ ID NOS: 19025
              Similarity
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SUGIYAMA, TOMOYASU
WAKAMATSU, AI
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Score 1646; DB 5;
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             APPLICATION
                         FILING DATE: 1997-09-1
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PRIOR APPLICATION NUMBER: 09/209,462
PRIOR FILING DATE: 1998-12-11
PRIOR APPLICATION NUMBER: CT/US98/1212
PRIOR APPLICATION NUMBER: CT/US98/1212
PRIOR FILING DATE: 1998-06-11
PRIOR PRIOR APPLICATION NUMBER: 60/049,547
PRIOR APPLICATION NUMBER: 60/049,548
PRIOR APPLICATION NUMBER: 60/049,548
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PRIOR APPLICATION NUMBER: 60/049,549
PRIOR APPLICATION NUMBER: 60/049,550
PRIOR APPLICATION NUMBER: 60/049,550
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PRIOR APPLICATION NUMBER: 60/049,566
PRIOR FILING DATE: 1997-06-13
PRIOR APPLICATION NUMBER: 60/049,606
PRIOR APPLICATION NUMBER: 60/049,607
PRIOR PFILING DATE: 1997-06-13
PRIOR APPLICATION NUMBER: 60/049,608
PRIOR APPLICATION NUMBER: 60/049,608
PRIOR APPLICATION NUMBER: 60/049,609
PRIOR FILING DATE: 1997-06-13
PRIOR APPLICATION NUMBER: 60/049,609
PRIOR APPLICATION NUMBER: 60/049,610
PRIOR FILING DATE: 1997-06-13
PRIOR APPLICATION NUMBER: 60/049,610
PRIOR APPLICATION NUMBER: 60/049,610
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PRIOR APPLICATION NUMBER: 60/049,611
PRIOR APPLICATION NUMBER: 60/049,611
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GENERAL INFORMATION:
APPLICANT: Rosen et
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                                              APPLICATION NUMBER: 60/051,919
FILING DATE: 1997-07-08
APPLICATION NUMBER: 60/055,984
                                                                                                                                                                               FILING DATE: 1997-06-13
APPLICATION NUMBER: 60/050,901
FILING DATE: 1997-06-13
                                                                                                                                APPLICATION NUMBER: 60/052,989 FILING DATE: 1997-06-13
FILING DATE: 1997-08-18 APPLICATION NUMBER: 60/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VEDPEYAVTQLAQTTMRSELGKLSXDKVFRERESLNASIVDAINQAADCWGIRCLRYEIK 178
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60/058,665
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NUMBER:

60/058,668

APPLICATION NUMBER: 60 FILING DATE: 1997-09-1 APPLICATION NUMBER: 60 FILING DATE: 1997-09-1

60/058,750

NUMBER: 60/058,669

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APPLICANT: Ghosh, Soumitra S.
APPLICANT: Faby, Eoin D.
APPLICANT: Zhang, Bing
APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: IDENTIFIED IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/060,844
PRIOR FILING DATE: 1997-10-02
PRIOR APPLICATION NUMBER: 60/060,865
PRIOR FILING DATE: 1997-10-02
PRIOR APPLICATION NUMBER: 60/061,059
PRIOR FILING DATE: 1997-10-02
PRIOR APPLICATION NUMBER: 60/061,060
                                                                                                                                                    Sequence 1904, Appli GENERAL INFORMATION:
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Best Local Similarity
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PRIOR APPLICATION NUMBER: 60/058,971
PRIOR FILING DATE: 1997-09-12
PRIOR APPLICATION NUMBER: 60/058,972
PRIOR FILING DATE: 1997-09-12
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                                                                                                                                                                                                                                                                  PSNPGDVTSMVAQAMGVYGALTKAPVPGTPDSLSSGSSRDVQGTDASXDEELDRVKMS 356
                                                                                                                                                                                                                                                                                                               PSNPGDVTSMVAQAMGVYGALTKAPVPGTPDSLSSGSSRDVQGTDASLDEELDRVKMS
                                                                                                                                                                                                                                                                                                                                                                                DIHVPPRVKESMQMQVEAERRKRATVLESEGTRESAINVAEGKKQAQILASEAEKAEQIN 238
                                                                                                                                                                                                                                                                                                                                                                                                  DIHVPPRVKESMQMQVEAERRKRATVLESEGTRESAINVAEGKKQAQILASEAEKAEQIN 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VEDPEYAVTQLAQTTMRSELGKLSXDKVFRERESLNASIVDAINQAADCWGIRCLRYEIK 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MLARAARGTGALLLRGSLLASGRAPR--RASSGLPRNTVVLFVPQQEAWVVERMGRFHRI 58
                                                                                                                                                                   Application US/60389987
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Pred. No. 1
 THERAPEUTIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 6;
1.9e-111;
                  INTERVENTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 356;
   PROTEOME
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; LENGTH: 356
; TYPE: PRT
; ORGANISM: Homo s
US-60-389-987-1904
                                                                                                                                                                                                                                                                                                       APPLICANT: Ghosh, Soumitra S.
APPLICANT: Fahy, Eoin D.
APPLICANT: Thang, Bing
APPLICANT: Chang, Bing
APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
APPLICANT: Glenn, Gary M.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: DENTIFIED IN THE MITOCHONDRIAL PROFILE REFERENCE: 660088.465P2
FILE REFERENCE: 660088.465P2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Qy
                                                                                                                                                            ; ORGANISM: Homo sapiens US-60-389-987-768
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US-60-389-987-768
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CURRENT FILING DATE: 2002-06-17
NUMBER OF SEQ ID NOS: 3025
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 768
LENGTH: 342
TYPE: PRT
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CURRENT FILING DATE: 2002-06-17
NUMBER OF SEQ ID NOS: 3025
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 1904
LENGTH: 356
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                                                                       Matches
                                                                                      Query Match
Best Local Similarity
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nes 340; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PSNPGDVTSMVAQAMGVYGALTKAPVPGTPDSLSSGSSRDVQGTDASLDEELDRVKMS
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                                                                       Conservative
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                                                                                      91.3%;
97.1%;
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95.0%;
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                                                                  Score 1613.5; DB Pred. No. 4e-109; 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1639; DB 7
Pred. No. 6e-111;
2; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 7;
                                                                                                                                                                                                                                                                                                                                                     INTERVENTION
                                                                                                     DB 7;
                                                                     4.
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                                                                     Indels
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                                                                                                      Length
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В

304 GDVTSMVAQAMGVYGALTKAPVPGTPDSLSSGSSRDVQGTDASLDEELDRVKMS

357

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APPLICANT: Zhang, Bing
APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PR
FILE REFERENCE: 660088.465P2
CURRENT APPLICATION NUMBER: US/60/389,987
CURRENT FILING DATE: 2002-06-17
NUMBER OF SEG ID NOS: 3025
SOFTWARE: FastSEQ for Windows Version 4.0
SEG ID NO 826
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GENERAL INFORMATION:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Ghosh,
APPLICANT: Fahy,
APPLICANT: Zhang,
                                                                                                                                                                                                                                                                                                                               TYPE: PRT
                                                                                                                                                                                                                                                                                                                                        LENGTH: 357
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                                                                                                                      EASAVLAKAKAKAEAIRILAAALTQHNGDAAASLTVAEQYVSAES
                                                                           KEGWEKGLRAPVEAERRKRATVLESEGTRESAINVAEGKKQAQII
                                                                                                                                                                                                                                                    332;
                                                      EASAVLAKAKAKAEAIRILAAALTQHNGDAAASLTVAEQYVSAFSKLAKDSNTILLPSNP
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RESULT 7
US-10-219-793-411
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PRIOR APPLICATION NUMBER: 60/049,566
PRIOR TILING DATE: 1997-06-13
PRIOR APPLICATION NUMBER: 60/049,606
PRIOR FILING DATE: 1997-06-13
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OR APPLICATION NUMBER: 60/055,984
OR FILING DATE: 1997-08-18
OR APPLICATION NUMBER: 60/058,665
OR FILING DATE: 1997-09-12
OR APPLICATION NUMBER: 60/058,668
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R APPLICATION NUMBER: 60/04
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OR APPLICATION NUMBER: 60/04
OR FILING DATE: 1997-06-13
                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 1997-06 APPLICATION NUMBER:
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FILING DATE: 1997-06-13
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APPLICATION NUMBER: 60/058,669
FILING DATE: 1997-09-12
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FILING DATE: 1997-06-13
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APPLICATION NUMBER: 60/049,608
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APPLICATION NUMBER: 60/061,060 FILING DATE: 1997-10-02 R OF SEQ ID NOS: 737
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FILING DATE: 1997-10-02
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APPLICATION NUMBER: 60/060,865
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APPLICATION NUMBER:
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SOFTWARE: PatentIn SEQ ID NO 411

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-219-793-411
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US-10-219-999-39902
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PRIOR FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 63520
SEQ ID NO 39902
LENGTH: 275
                                                                                                                     Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                APPLICANT: Stein, Joshua
TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-10(52726)C
CURRENT APPLICATION NUMBER: US/10/219,999
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: US 60/324,109
PRIOR FILING DATE: 2001-09-21
PRIOR FILING DATE: 2001-09-21
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                                                                                                                                                                                                              TYPE: PRT
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              160 AINQAADCWGIRCLRYEIKDIHVPPRVKESMQMQVEAERRKRATVLESEGTRESAINVAE 219
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nes 304; Conserv
                                                                                                       Local Similarity
mes 131; Conserv
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Hinkle, Gregory J.
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99.3%;
                                                                                                     35.1%; Score 619.5; DB 6; 48.2%; Pred. No. 4.1e-37; tive 47; Mismatches 77;
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Pred. No. 1.9e-100;
Mismatches
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GENERAL INFORMÁTION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Grego
APPLICANT: Kovalle, Davi
APPLICANT: Liu, Jingdong
APPLICANT: Stein, Joshua
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US-10-219-999-55341
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PRIOR APPLICATION NUMBER: US 60/312,544
PRIOR FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 63520
SEQ ID NO 55341
LENGTH: 283
TYPE: PRT
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Best Local Similarity
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APPLICANT: Edgerton, Nichael
APPLICANT: Hinkle, Gregory J.
APPLICANT: Kovalic, David K.
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CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: US 60/324,109
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APPLICANT: Stein, Joshua
TITLE OF INVENTION: cDNA SEQUENCES AND USES
FILE REFERENCE: 38-10(52726)C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72 APALSRSFSRFNPRDDSSMFDPPEPPVNWGYSIVPEKKAYVVERFGKYLKTLGSGFHLLI 131
                                                                                                                                                                                                                                                                                                                                                                                                                                           PVLDRIRYVQSLKEIVINVPEQSAVTLDNVTLQIDGVLYLRIMDPYKASYGVEDPEYAVT 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GKKTAQILESEGAMLDLANRAKGAAEAILAKSEATARGMRLVSDAMTTEGSAKAASLKLA
                                                                                                                                                                                                                                                                                                                                         QLAQTTMRSELGKITLDKTFEERDALNEKIVSAINEAATDWGLKCIRYGIRDINPPAGIR
                                                                                                                                                                                                                                                                                                                                                                             QLAQTTMRSELGKLSXDKVFRERESLNASIVDAINQAADCWGIRCLRYEIKDIHVPPRVK 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -VPGTPDSLSSGSSRDVQGTDASXDEELDRVK 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EQYIEAFSNLAQKTNTMLLPGDSASPASFVAQAMKTYEQIHSHSQALKSHPQIEELKESG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AINEAATDWGLKCIRYEIRDINPPAGIRQAMEMQAEAERKKRAQILESEGMKQAQILESE
INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
                                                      Edgerton, Michael D
Hinkle, Gregory J
Kovalic, David K.
                  Liu, Jingdong
Stein, Joshua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32.7%; Score 578.5; DB 53.4%; Pred. No. 4e-34;
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                                                                                                                                                                                                                                                              EGMKQAQILESE
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; SEQ ID NO 51693
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Zea mays
US-10-219-999-51693
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; Sequence 6, Application US/09898216
; GENERAL INFORMATION:
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Best Local Similarity
Matches 123; Conserv
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CURRENT APPLICATION NUMBER: US/10/219,999
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: US 60/324,109
PRIOR FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: US 60/312,544
PRIOR FILING DATE: 2001-08-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   335 SSRDVQGTDASXDEELDRVK 354
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                                                                                                                                                                        COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEO FOR Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/898,216
FILING DATE: 02-Jul-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0181 US
TELECOMMUNICATION INFORMATION:
                                                                                                           PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/781,562

FILING DATE: <Unknown>
                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
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47.3%; Pred. No. 8.4e-34;
tive 44; Mismatches 76;
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US-09-791-537-98751
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                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 98751
LENGTH: 305
TYPE: PRT
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Best Local Similarity
Matches 110; Conserv
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Best Local
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APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Bionomix, Inc.
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           323 EPSPVEDQPKHAADGDDAEVAGWFSTDTDPS 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          218 AEGKKQAQ------ILASEAEKAEQINQAAGEASAVLAKAKAKAEAIRILAAALT 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      206 AEGOKOAQILAAEGAKOAAILAAEADRQSRMLRAQGERAAAYLQAQGQAKAIEKTFAAI- 264
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                  38 VLFVPQQEAWVVERMGRFHRILEPGLNILIPVLDRIRYVQSLKEIVINVPEQSAVTLDNV 97
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                                                                                                Local Similarity
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VDAINQAADCWGIRCLRYEIKDIHVPPRVKESMQMQVEAERRKRATVLESEGTRESAINV 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TLNIDTVVYFQVTVPQAAVYEISNYIVGVEQLTTTTLRNVVGGMTLEQTLTSRDQINAQL 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TLQIDGVLYLRIMDPYKASYGVEDPEYAVTQLAQTTMRSELGKLSXDKVFRERESLNASI 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -- KAGRPTPEMLAYQYLQTLPEMARGDANKVWVVPSDFNAALQGFTRLLGKPGEDGVFRF
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                                                                               Conservative
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                                                                                            26.4%;
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                                                                               76;
                                                                             Score 466; DB 5;
Pred. No. 6.5e-26;
6; Mismatches 94;
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                                                                                                                   Length 305;
                                                                               Indels
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RESULT 13
US-09-602-777A-140
; Sequence 140, Application US/09602777A
; GENERAL INFORMATION:
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TITLE OF INVENTION: CORVNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
TITLE OF INVENTION: INVOLVED IN HOMEOSTASIS AND ADAPTATION
FILE REFERENCE: BGI-128CP
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               OR FILING DATE: 1999-07-14
OR APPLICATION NUMBER: DE 19933003.4
OR FILING DATE: 1999-07-14
OR APPLICATION NUMBER: DE 19933005.0
OR FILING DATE: 1999-07-14
OR APPLICATION NUMBER: DE 19933006.9
OR FILING DATE: 1999-07-14
OR APPLICATION NUMBER: DE 19941378.9
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                                                                                                                                                                                      FILING DATE: 1999-07-14
APPLICATION NUMBER: DE 19932973.7
FILING DATE: 1999-07-14
APPLICATION NUMBER: DE 19933002.6
                                                                                                                                                                                                                                                                       APPLICATION NUMBER: DE 19932935.4
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: DE 19932924.9 FILING DATE: 1999-07-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: DE 19932920.6 FILING DATE: 1999-07-14
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APPLICATION NUMBER: DE 19932128.0
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APPLICATION NUMBER: DE 19932126.4
                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: DE 19932933.8 FILING DATE: 1999-07-14
                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: DE 19932930.3 FILING DATE: 1999-07-14
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                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: DE 19932928.1
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Zelder, Oskar
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DATE:
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                                                                                                                                                                              ; ORGANISM: Aquifex aeolicus US-09-791-537-75409
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LENGTH: 432
TYPE: PRT
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 75409
LENGTH: 253
TYPE: PRT
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APPLICANT: Bionomix, Inc.
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Best Local Similarity
Matches 112; Conserv
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                                                                                               Query Match
Best Local Similarity
                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: DE 19941391.6
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: DE 19942088.2
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 442
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PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: DE 19941390.8
PRIOR FILING DATE: 1999-08-31
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15 VLLFLASAIKVIPEYERAVVFRLGRVIGAKGPGLIIVIPIIDRIVRV-SLRTVTLDVPTQ 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AEGKKQAQILASEAEK------AEQ---INQAAGEASAVLAKAKAKAEAIRILAAALT 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QHNGDAAASLT---VAEQYVSAFSKLAKD--SNTILLPSNPGDVTSMVAQAMGVYGALTK 321
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                                                                                               21.3%; Score 376.5; DB 5 39.3%; Pred. No. 1.6e-19;
                                                                          47;
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                                                                               Mismatches
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CURRENT APPLICATION NUMBER: US/09/458,180
CURRENT FILING DATE: 1999-12-08
PRIOR APPLICATION NUMBER: US 08/895,611
PRIOR FILING DATE: 1997-07-16
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
SEQ ID NO 2
LENGTH: 576775
TYPE: PT
ORGANISM: Aquifex aeolicus
US-09-458-180-2
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US-09-458-180-2
Search completed: September 22, 2002, 18:30:32 Job time: 635 sec
                                                                                                                       Db 553601 EYQAAQKLLEA---ARILAGE 553618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09458180
GENERAL INFORMATION:
APPLICANT: DIVERSA CORPORATION
APPLICANT: Swanson, Ronald V.
APPLICANT: Swanson, Ronald V.
APPLICANT: Short, Jay M.
TITLE OF INVENTION: NUCLEOTIDE SEQUENCE OF THE AQUIFEX
TITLE OF INVENTION: AEGLICUS GENOME, FRAGMENTS THEREOF, AND USES THEREOF
FILE REFERENCE: DIVER1330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 21.3%; Score 376.5; DB 5; Length 576775; Best Local Similarity 39.3%; Pred. No. 4e-15; Matches 79; Conservative 47; Mismatches 64; Indels 11; Gaps
                                                                                                                                                   210 TRESAINVAEGKKQAQILASE 230 ::| : | |:||| |
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74 DVITKDNVTVQVDAVVYFRVVDPVKAIVEVEDYFYATSQIAQTTLRSVCGEAELDELLSQ 133
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Post-processing: Minimum Match 0%
Maximum Match 100%
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Perfect score:
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E87667
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(without alignments)
767.163 Million cell updates/sec
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A:Map position: 9
A:Introns: 2/3; 48/3; 82/1; 101/3; 135/3; 194/3; 243/1; 269/3; 312/3 C:Superfamily: erythrocyte band 7 integral membrane protein

RESULT 1  T02246  C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Accession: T02246 A;Roteses: T02246 A;Roteses: T02246 A;Roteses: T02246 A;Roteses: T02246 A;Roteses: T02246 A;Roteses: T02546 A;Roteses: T0254	ALIGNMENTS	30 442.5 25.0 322 2 A97030 31 423.5 24.0 305 2 E72322 32 417.5 23.6 392 2 G84191 33 412 23.3 309 2 D90520 34 52 21.3 25.3 25.3 25.3 25.3 25.3 25.3 25.3 25
1999 #text_change 11-Jan-2000 E.; Adamson, A.W.; Burkhart-Schultz, K. Liu, S.; Attix, C.; Andreise, T.; Trank homas, P.; Quan, G.; Kronmiller, B.; Ar clone containing the XRCC9 DNA repair		membrane protease conserved hypothet hypothetical prote conserved hypothet erythrocyte band 7 hypothetical prote membrane protein h probable erythrocy stomatin-like prot probable stomatin- probable stomatin- probable stomatin- hypothetical prote stomatin-like prot erythrocyte band 7

Š 밁 Ωy DЬ Qy В γΩ DЬ δÃ В δÃ Query Match Best Local S Matches 332 304 303 184 194 124 137 64 77 17 6 QSLKEIVINVPEQSAVTLDNVTLQIDGVLYLRIMDPYKASYGVEDPEYAVTQLAQTTMRS ------VEAERRKRATVLESEGTRESAINVAEGKKQAQILASEAEKAEQINQAAG KEGWEKGLRAPVEAERRKRATVLESEGTRESAINVAEGKKQAQILASEAEKAEQINQAAG al Similarity 332; Conser 90.8%; nilarity 93.8%; Conservative Score 1605; DB 2; Pred. No. 2.9e-98; 2; Mismatches 4 2: Length 357; Indels 16; Gaps 183 193 123 243 242 303 2

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R.Barlow, K.
submitted to the EMBL Data Library, October 1996
A.Reference number: 219442
A.Accession: T21562
A.Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein F30A10.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C:Accession: T21562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A:Map position: 1
A:Introns: 16/2; 68/3; 124/3; 227/2
C:Superfamily: erythrocyte band 7 integral membrane protein
                                                                                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-334 <WIL>
A; Cross-references: EMBL: Z81072; PIDN: CAB03018.1;
A;Gene: SPDB:SPBC16G5.07c
A;Map position: 2
A;Introns: 72/2; 265/2
C;Superfamily: erythrocyte
                                                                            A; Experimental source: C; Genetics:
                                                                                                                  A; Molecule type: DNA
A; Residues: 1-354 <LYN>
A; Cross-references: EMB
                                                                                                                                                                                             C:Accession: T39599
R:Lyne, M.: Wood, V.: Rajandream, M.A.: submitted to the EMBL Data Library, May A;Reference number: Z21866
A;Accession: T39599
                                                                                                                                                                                                                                                                                         conserved hypothetical protein SPBC16G5.07c - fission yeast (Schizosaccharomyces
C; Species: Schizosaccharomyces pombe
C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 18-Feb-2000
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                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local Similarity
Matches 188; Conserv
    Superfamily: erythrocyte
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VEAERKKRAAILESEGIREAAINRAEGDKKSAILASEAVQAERINVAKGEAEAVILKAES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VEAERRKRATVLESEGTRESAINVAEGKKQAQILASEAEKAEQINQAAGEASAVLAKAKA 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MRSEVGKINLDTVFKERELLNENIVFAINKASAPWGIQCMRYEIRDMQMPSKIQEAMQMQ 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MRSELGKLSXDKVFRERESLNASIVDAINQAADCWGIRCLRYEIKDIHVPPRVKESMQMQ 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QSLKEIVINVPEQSAVTLDNVTLQIDGVLYLRIMDPYK---ASYGVEDPEYAVTQLAQTT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSTLPLAVTSSRQAHAAHNTVINFVPQQEAWVVERMGKFYKILEPGLNFLLPIIDKIKFV 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSGLP-----RNTVVLFVPQQEAWVVERMGRFHRILEPGLNILIPVLDRIRYV 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RAKAIERIALALEKDGGANAAGLTVAEQYVGAFGNLAKESNTVVLPANLSDPGSMVSQAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QNLREIAIEIPEQGAITIDNVQLRLDGVLYLRVFDPYKACDASYGVDDPEFAVTQLAQTT 143
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                                                                                                                    EMBL: AL023554;
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                                                                                              strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54.2%; Score 957.5; DB 2; 61.2%; Pred. No. 9.6e-56;
  band 7 integral membrane protein
                                                                                                972h-;
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                                                                                                                  PIDN:CAA19027.1;
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                                                                                                                    GSPDB:GN00067;
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                                                                                                                    SPDB:SPBC16G5.07c
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A; Molecule type: DNA
A; Residues: 1-515 <BEV>
A; Cross-references: EMBL: AL035602
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A; Note: T29A15.70
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Best Local Similarity
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INVAEGKKQAQILASEAEKAEQINQAAGEASAVLAKAKAKAEAIRILAAAL-TQHNGDAA 273
                                                                    ILAAALTQHNGDAAASLTVAEQYVSAFSKLAKDSNTILLPSNPGDVTSMVAQAMGVYGAL 319
                                                                                                                                                                  KITLDKTFEERDTLNEKIVEAINVAAKDWGLQCLRYEIRDIMPPHGVRAAMEMQAEAERK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VSLYIAQQYITNFGKLAKASNSMIVPASTSDVSGMVAQALSIFKQVSKTTAPDKSTPKEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ASIVDAINQAADCWGIRCLRYEIKDIHVPPRVKESMQMQVEAERRKRATVLESEGTRESA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNVTLQIDGVLYLRIMDPYKASYGVEDPEYAVTQLAQTTMRSELGKLSXDKVFRERESLN
                                                                                                                          KRATVLESEGTRESAINVAEGKKQAQILASEAEKAEQINQAAGEASAVLAKAKAKAEAIR 259
                                                                                                                                                                                         KLSXDKVFRERESLNASIVDAINQAADCWGIRCLRYEIKDIHVPPRVKESMQMQVEAERR 199
                                                                                                                                                                                                                        KEEAIPIPNQTAITKDNVSIHIDGVLYVKIVDPKLASYGVESPIYAVVQLAQTTMRSELG
                                                                                                                                                                                                                                                                              SAGYPSNSFQLTPPTNWGIRIVPERKAFVIERFGKYATTLPSGIHFLIPFVDRIAYVHSL 104
                                                                                                                                                                                                                                                                                                      SSGLPRNTVVL-----FVPQQEAWVVERMGRFHRILEPGLNILIPVLDRIRYVQSL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INVAEGDKQAEILDSEGQKIKTINSALAEAQAIREKASATASGIAVLADSIKKQEHGLEA
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                                                                                                                                                                                                                                                 KEIVINVPEQSAVTLDNVTLQIDGVLYLRIMDPYKASYGVEDPEYAVTQLAQTTMRSELG 139
                            TKAPVPGTPDSLSSGSSRDVQGTDASXDEELDRVK
                                                   LLSQSLKETGGVEAASLRVAEQYITAFGNIAKEGTIMLLPSGASNPASMIAQALTMYKSL
                                                                                                           KRAQILESEGERQSHINIADGKKSSVILASEAAKMDQVNRAQGEAEAILARAQATAKGLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          170;
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-VINGPSKDHQETQALDETDLEELE
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56:7%;
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50.18;
                                                                                                                                                                                                                                                                                                                                   67;
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Pred. No. 7.5e
57; Mismatches
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Pred. No. 2.1e-49
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.5e-47;
 368
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hypothetical protein RC0452 [imported] - Rickettsia conorii (strain Malish C;Species: Rickettsia conorii C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 22-Oct-2001 C;Accession: D97756 R;Ogata, H; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; S; Science 293, 2093-2098, 2001 Science 293, 2093-2098, 2001 A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowa: A;Reference number: A97700; MUID:21442074; PMID:11557893 A;Accession: D97756
                                                                                                                                                                                                                                                                                                                                      hypothetical protein RP328 - Rickettsia prowazekii C:Species: Rickettsia prowazekii C:Species: Rickettsia prowazekii C:Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000 C:Accession: B71689 C:Accession; Signature 36, 20morodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T. Nature 396, 133-140, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
B71689
                                                                                                                                         A;Gene: RP328 C;Superfamily: erythrocyte band 7 integral membrane
                                                                                                                                                                                             A;Cross-references: GB:AJ235271; GB:AJ235269; NID:g3868717; PIDN:CAA14788.1; PID:g386080
A;Experimental source: strain Madrid E
                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-311 <AND>
                                                                                                                                                                                                                                                                                   A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria A;Reference number: A71630; MUID:99039499
A;Accession: B71689
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A; Residues: 1-312 <KUR>
                                                                                                                                                                                                                                                                 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
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                                                     Query Match
Best Local S
Matches 154
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Best Local S
Matches 158
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                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VAEGKKQAQILASEAEKAEQINQAAGEASAVLAKAKAKAEAIRILAAALTQHNGDAAASL 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IVAAINQAAINWGIQCMRYEIKDIQPPQTILKAMELQVAAERQKRAQILESEGNRQAKIN
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 Conservative
                                                       Conservative
                                                                     45.6%;
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54.3%;
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                                                 Score 806; DB 2;
Pred. No. 7.9e-46;
0; Mismatches 69
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Pred. No. 3.
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                                                       69;
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                R; Parkhill, J.; Achtman, M.; James, Holroyd, S.; Jagels, K.; Leather, Nature 404, 502-506, 2000
                                                                probable periplasmic protein NMA1382 [imported] - Neisseria meningitidis (strain C;Species: Neisseria meningitidis C;Species: Neisseria meningitidis C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001 C;Accession: H81907
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 A;Title:
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hypothetical protein C0800w - malaria parasite (Plasmodium falciparum) c;Species: Plasmodium falciparum c;Species: Plasmodium falciparum C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun C;Accession: T18493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references:
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-374 <LAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Lawson, D.; Bowman, S.; Barrell, submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
T18493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Map position:
A; Note: C0800w
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A; Accession: T18493
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Best Local Similarity
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    291
                                       261
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ISNKIKKLDSNNAISLLVAEQYIDVFSNICKNNNTVIIPADLNNISSLISQSLSIY
                                                                                                RATVLESEGTRESAINVAEGKKQAQILASEAEKAEQINQAAGEASAVLAKAKAKAEAIRI
                                                                                                                                                                             LSXDKVFRERESLNASIVDAINQAADCWGIRCLRYEIKDIHVPPRVKESMQMQVEAERRK
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                                     LAAALTQHNGDAAASLTVAEQYVSAFSKLAKDSNTILLPSNPGDVTSMVAQAMGVY 316
                                                                              RAEILQSEGERESEINIAIGKKRKSILIAE-----
                                                                                                                                                        LTLDATFLERDNLNEKLYKAINESAKNWGIKCMRYEIRDIILPVNIKNAMEKQAEAERRK
                                                                                                                                                                                                                                      EETITIPNQTAITKDNVTLNIDGVLYIKCDNPYNSSYAIEDAVFAVTQLAQVTMRSELGK
                                                                                                                                                                                                                                                                           EIVINVPEQSAVTLDNVTLQIDGVLYLRIMDPYKASYGVEDPEYAVTQLAQTTMRSELGK 140
                                                                                                                                                                                                                                                                                                                    FWNHLG-----FVIIPQETAYIVERLGKYNKTLLAGIHFLIPFIDKIAYVFSLK
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                                                                                                                                                                                                                                                                                                                                                                                                                 46.68;
                                                                                                                                                                                                                                                                                                                                                                                               68;
                                                                                                                                                                                                                                                                                                                                                                                                                 Score 722; DB 2;
Pred. No. 3.4e-40;
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                                                                              -GQSFAIKAKADATAEAIEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 374;
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Complete DNA sequence of a

K.D.; Bentley,
S.; Moule, S.;

S.D.; Churcher, C.; Klee,
Mungall, K.; Quail, M.A.;

S.R.; Mo Rajandre

Z249

Z2491

serogroup A strain of Neisseria menigitidis

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stomatln/Mec-2 family protein NMB1220 [imported] - Neisseria meningitidis (strain MC58 C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C;Accession: F81107
R;Tettelin, H:; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.R;Tettelin, H:; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.R; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O:; Fleischmann, R.D.; Dougherty, B.P. ri, H:; Qin, H:; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A;Title: Complete genome sequence of Neisseria meningilidis serogroup B strain Mc58.
A;Reference number: A81000; MUID:20175755
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A:Experimental source: serogroup
C:Genetics:
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A;Molecule type: DNA
A;Residues: 1-315 <PAR>
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C; Superfamily:
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A; Residues: 1-315 <TET>
A; Cross references: GB: AE002470;
A; Experimental source: serogroup
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Best Local S
Matches 140
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                                                                                                                                                   VPQQEAWVVERMGRFHRILEPGLNILIPVLDRIRYVQSLKEIVINVPEQSAVTLDNVTLQ 100
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                                                                                                                                                                                                  140;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAEREKRARIAESEG
                        VDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIGRMELDKTFEERDEINSTVVAA
                                                                                                             IPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSLKEIPLDVPSQVCITRDNTQLT 81
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                                                                                                                                                                                                56;
                                                                                                                                                                                                                                                                                                                                                                   GB:AE002098; NID:97226457; PIDN:AAF41602.1; B, strain MC58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GB:AL157959; NID:g7379742; PIDN:CAB84628.1; PID:g738005
A, strain Z2491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 716; DB 2;
Pred. No. 6.6e-40;
                                                                                                                                                                                                               Score 712.5; DB:
Pred. No. 1.1e-39
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                                                                           C;Accession: D75311
C;Accession: D75311
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E
M.; Shen, M.; Vamathevan, J.J.; Lam, P. S.; Smith, H.O.; Venter, J.C.; Fraser, C. Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresi A;Reference number: A75250; MUID:20036896
                                                                                                                                                 conserved hypothetical protein - Deinococcus radiodurans (strain
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change
                                                                                                                                                                                                                    D75311
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j

the radioresistant bacterium Deinococcus  $\mbox{\sc MUID:}\,20036896$ 

radiodurans

#text\_change 17-Mar-2000

R1)

E.K.; Peterson, J.D.; Dodson, L.; Utterback, T.; Zalewski,

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DNA Res.
A; Title:
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A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #
C:Accession: S74505
R.Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asan o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, DNA Res. 3, 109-136, 1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-321 <K/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: S74322; A; Accession: S74505
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Best Local Similarity
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258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GADAVNIKIAEQYVAAFNNLAKESNTLIMPANVADIGSLISAGMKI 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLRLVAEANAEAIRQIAAALQTQG
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QFLLAQQYLNMGTTIGSSDSSKVMFLDPRNILSTLEGVRSIVG
                                   SLTVAEQYVSAFSKLAKDSNTILLPSNPGDVTSMVAQAMGVYG
                                                                         NSAQGDAQARVLEAEAKKKAAILNAEAEQQKKVLEAKATAEALSILTEKLSSDNHAREAL
                                                                                                            NVAEGKKQAQILASEAEKAEQINQAAGEASAVLAKAKAKAEAIRILAAALTQHN-GDAAA 274
                                                                                                                                                    LLLRELDISTOPWGVKVTRVELRDIMPSKAVLDSMELQMTAERKKRAAILTSEGQRDSAI
                                                                                                                                                                                       SIVDAINQAADCWGIRCLRYEIKDIHVPPRVKESMQMQVEAERRKRATVLESEGTRESAI 215
                                                                                                                                                                                                                               NVAITADAVVYWRIIDMEKAYYKVENLQSAMVNLVLTQIRSEIGKLELDQTFTARTEINE 137
                                                                                                                                                                                                                                                                NVTLQIDGVLYLRIMDPYKASYGVEDPEYAVTQLAQTTMRSELGKLSXDKVFRERESLNA 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GDAAASLTVAEQYVSAFSKLAKDSNTILLPSNPGDVTSMVAQAMGV 315
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Pred. No. 1.2e-25;
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T.; Watanabe,
 300
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Conserved hypothetical protein XF0185 [imported] - Xylella fastidiosa (strain 9a5c) C;Species: Xylella fastidiosa (C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_charge 02-Sep-2000 C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_charge 02-Sep-2000 C;Accession: A82838 R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen Nature 406, 151-157, 2000 A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A;Reference number: A82515; MUID:20365717 A;Note: for a complete list of authors see reference number A;59328 below
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A; Residues: 1-344 < WHID
A; Cross-references: GB: AE002048;
A; Experimental source: strain Rl
C; Genetics:
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A; Status: preliminary
                                                               M.; Tsuhako, M.H.; Vallada, H.; A; Reference number: A59328
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C: Superfamily: erythrocyte
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                                               A; Contents: annotation
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A; Residues: 1-337 <SIM>
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Best Local s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QQYVEALRDVASAPNQKTLILPI - - - EATSILGSLQGIAEVAKEAFTPGS
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Pred. No. 1.9e
67; Mismatches
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R.Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Ko n, J.; Ermolaeva, M.; White, O.; Salzberg; S.L.; Shapiro, L.; Venter, J.C.; Fraser, C Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: E87667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            band 7/Mec-2 family protein [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C;Accession: E87667
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A; Residues: 1-310 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Superfamily: erythrocyte band 7 integral membrane proteir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: CC3375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: GB: AE005673; NID: g13425081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 107; Conserv
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Best Local
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                                                                                                                                                                                                                                                                                                                                                 SAIKIVPQGREFTVERFGRYTRTLKPGITILTPFLETVGRRVNMMEQVLDVPQQEVITKD
                                                                                                                                                                                                                                                                                                                                                                            TVVLFVPQQEAWVVERWGRFHRILEPGLNILİPVLDRIRYVQSLKEIVINVPEQSAVTLD:: | | : | | : | | : | | : | | : | | : | |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YVQSLKEIVINVPEQSAVTLDNVTLQIDGVLYLRIMDPYKASYGVEDPEYAVTQLAQTTM 134
                      SLTVAEQYVSAFSKLAK -- DSNTILLPSNPGDVTSMVAQAMGVYGALTK----
                                                                                                              NVAEGKKQAQILASEAEKAEQINQAAGEASAVLAKAKAEAIRILAAALTQHNGDA-AA
                                                                                                                                                                                                                                                         NVSVKVDATVFIQVMDAAAAAYRVDNLMYATTQLAQTNLRTVVGAMELDEVLSQRDAINS
                                                                                                                                                                                                                                                                                 NVTLQIDGVLYLRIMDPYKASYGVEDPEYAVTQLAQTTMRSELGKLSXDKVFRERESLNA 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -GI-ADLTREAL-GKSDHSATPSQRPHRG 337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AEAIRILAAALTQHNGDAAASLTVAEQYVSAFSKLAKDSNT--ILLPSNPGDVTSMVAQA
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                                                                    ARAEGQKQSAILQAEGRR----EAAFRDAEAREREAEAEAKATAFVSEAIAK--GDVNAI
                                                                                                                                                              RLLSTIDHATGPWGVKVARIEIKDLTPPADITNAMARQMKAERERRAVITEAEGEKQAQI
                                                                                                                                                                                                          SIVDAINQAADCWGIRCLRYEIKDIHVPPRVKESMQMQVEAERRKRATVLESEGTRESAI 215
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35.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                79;
Score 486; DB 2;
Pred. No. 8.5e-25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 310;
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                      -APVPGT
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A;Cross-references: GB:AL590842; PIDN:CAC92325.1; PID:g15981036; GSPDB:GN00175 C;Genetics:
                                                                                                                                                                                                                               conserved hypothetical protein YPO3083 [imported] - Yersinia pestis (strain CO92) C;Species: Yersinia pestis
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C;Accession: AB0375
R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Li, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
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AB0375
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A;Residues: 1-322 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB74171.1; PID:g17131564; GSPDB:GN00179
A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Reza, B., 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AI2114
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AI2114
hypothetical protein alr2472 [imported] - Anabaena sp. (strain PCC 7120)
C:Species: Anabaena sp.
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                                                           A; Molecule type: DNA
A; Residues: 1-304 <KUR>
                                                                                                                                           A;Title: Genome sequence of Yersinia pestis, the causative agent of plague. A;Reference number: AB0001; MUID:21470413; PMID:11586360 A;Accession: AB0375
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C;Superfamily: erythrocyte band 7 integral membrane protein
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                                                                                                                 A; Status: preliminary
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Genetics:
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  261 SNGTAEQALEVLLALGYLDMGATTGKSDSSKVMFMDPRAIPATLEGIRSIVSDS 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         y Match 27.3%; Score 482.5; DB 2; Local Similarity 37.1%; Pred. No. 1.5e-24; hes 109; Conservative 67; Mismatches 99;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VKVINGGNEVLVERLGSYHKKLGPGLNLVLPFIDKAVYKETIREKVLDIPPOKCITRDNV 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HNGDAAASLTV--AEQYVSAFSKLAK-DSNTIL-----LPSNPGDVTSMVAQA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARGKAEAQILDAEARQKSVILQAEAEQKAIVLKAQAERQQQVLKAQAIAESAEILAQKIS
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A;Gene: xp03083
C;Superfamily: erythrocyte band 7 integral membrane protein
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Matches 99; Conservative
                                    275 SLTVAEQYVSAFSKL--AKDSNTILLPSNPGDVTSMVAQAMGVYGALTK 321
                                                                                                                216 NVAEGKKQAQILASEAEKAEQINQAAGEASAVLAKAKAKAEAIRILAAALTQHNGD-AAA 274
                                                                                                                                                         138 RLLHIVDEATNPWGIKITRIEIRDVRPPTELISAMNAQMKAERTKRADILEAEGVRQAAI 197
                                                                                                                                                                                                156
252 NYFVAQKYTDALQHIGSANNSKVIMMPLE-----ASSLMGAIGGIAE
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                                                                                                                                                                                                                                                                                                                                                        36 TVVLFVPQQEAWVVERMGRFHRILEPGLNILIPVLDRIRYVQSLKEIVINVPEQSAVTLD 95
                                                                                                                                                                              SIVDAINQAADCWGIRCLRYEIKDIHVPPRVKESMQMQVEAERRKRATVLESEGTRESAI 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                Length 304;
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Search completed: September 22, 2002, 18:22:45 Job time: 3402 sec

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Listing first 45 summaries
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                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2000 Com
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FLT1_RAT
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NVTLQIDGVLYLRIMDPYKASYGVEDPEYAVTQLAQTTMRSELGKLSXDKVFRERESLNA 155

NVAITADAVVYWRIIDMEKAYYKVENLQSAMVNLVLTQIRSEIGKLELDQTFTARTEINE

Query Match 28.3%; Best Local Similarity 37.1%; Matches 105; Conservative 67

67;

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                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg
Delcher A., Utterback T., Weldman J., Khouri H., Gill J., Mikula
                                 TubercuList; Rv1488; -...
InterPro; IPR001107; Band_7.
InterPro; IPR001972; Stomatin
Pfam; PF01145; Band_7; 1.
SMART; SM00244; PHB; 1.
                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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16-OCT-2001 (Rel. 40, Last annotation
Hypothetical 41.2 kDa protein RV1488.
RV1488 OR MT1533.2 OR MTCY277.09.
                   PROSITE;
                                                                                                                    EMBL; AE007022; AAK45800.1; -. TIGR; MT1533.2; -.
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE BAND 7 / MEC-2 FAMILY.
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ein; Transmembrane;
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STRAIN-K12 / MG1655;
MEDLINE-9742661T; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A.
Riley M., Collado-Vides J., Glasner J.D.,
Gregor J., Davis N.W., Kirkpatrick H.A., (
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SEQUENCE
          Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
                                                                                                                                  Roberts D., Allen E., Araujo K., Apartico ..., Comp C., Duncan M., Federspiel N., Hyman R., Kalman S., Komp C., Lew H., Lin D., Namath A., Oefner P., Schramm S., Davis
                                                                                                                                                                                                                                                                                                                                                                                                                           YBBK_ECOLI STANDARD; PRT; 3
977367;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
Hypothetical protein ybbK.
YBBK OR B0489 OR 20642 OR ECS0552.
                                                                              STRAIN=0157:H7 / EDL933 / ATCC 700 MEDLINE=21074935; PubMed=11206551;
                                                                                                                                                                                                                       "The complete genome sequence Science 277:1453-1474(1997).
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                                                                                                           SEQUENCE
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026788;
30-MAY-2000
30-MAY-2000
16-OCT-2001
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Hypothetical protein; Transmembrane; Complete proteome TRANSMEM 3 23
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InterPro; IPR001107; Band_7.
InterPro; IPR001972; Stomatin.
Pfam; PF01145; Band_7; 1.
SMART; SM00244; PHB; 1.
Methanobacterium thermoautotrophicum
                                  Hypothetical MTH692.
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MEDLINE-21156231; PubMed-11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K.,
Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M.,
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Pred. No. 2.2e-23;
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MEDLINE-98037514; PubMed-9371463;
Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
"Complete genome sequence of Methanobacterium thermoautotrophicum deltaH: functional analysis and comparative genomics.";
J. Bacteriol. 179:7135-7155(1997).
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Hypothetical protein; Transmembrane; Complete proteome TRANSMEM 2 22 POTENTIAL.
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Hypothetical protein; Transmembrane; Complete proteome
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                                                                                                                                                        EYQAAMKLREA---ADVLA-QSEGAILLRYLQTLNEISAEQNTTI
                                                                                                                                                                                          TRESAINVAEGKKQAQILASEAEKA-----EQINQAAGEASAVL 248
                                                                                                                                                                                                                                                            RESLNASIVDAINQAADCWGIRCLRYEIKDIHVPPRVKESMQMQVEAERRKRATVLESEG
                                                                                                                                                                                                                                                                                              EVVTKDNVTVKVNAVVYYRVVDPAKAVTEVFDYQYATAQLAQTTLRSIIGQAELDEVLSE 130
                                                                                                                                                                                                                                                                                                                              SAVTLDNVTLQIDGVLYLRIMDPYKASYGVEDPEYAVTQLAQTTMRSELGKLSXDKVFRE 149
                                                                                                                                                                                                                                                                                                                                                                 VVLFLLSAVRIVKEYERGVIFRLGRLVGARGPGLFFIIPILENM-VVVDLRTVTYDVPSQ 70
                                                                                                                                                                                                                                                                                                                                                                                                VVLF-----VPQQEAWVVERMGRFHRILEPGLNILIPVLDRIRYVQSLKEIVINVPEQ 89
                                                                                                                                                                                                                            RDKLNVKLQQIIDEETNPWGIKVTAVEIKDVELPEEMRRIMAMQAEAERERRSKIIRAEG
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Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
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   (Rel. 35,
(Rel. 35,
(Rel. 40,
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                                                                     STANDARD;
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Last annotation updat
                                   Created)
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Pred. No. 8.5e-17
0; Mismatches 7
                                                                       PRT;
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Matches 67
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MEDLINE=96337999; PubMed=8688087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus

jannaschi."
                                                                                                30-MAY-2000
30-MAY-2000
16-OCT-2001
ALCHAea; Euryarchaeota;
NCBI_TaxID=53953;
[1]
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                                                                   Hypothetical PH1511.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein; Transmembrane; Complete proteome TRANSMEM 7 27 POTENTIAL. SEQUENCE 199 AA; 22809 MW; 2545CE07DD54337E CRC64;
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InterPro; IPR001972; Stomatin.
Pfam; PF01145; Band_7; 1.
SMART; SM00244; PHB; 1.
SMART; SM00244; PHB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     between the Swiss Institute of Bioinformatics and the EMBL outst
the European Bioinformatics Institute. There are no restrictions
use by non-profit institutions as long as its content is in
modified and this statement is not removed. Usage by and for com-
entities requires a license agreement (See http://www.isb-sib.ch/an
                                                                                                                                                  YF11_PYRHO 059180;
                                                                                                                                                                                  PYRHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U67526; AAB98826.1; TIGR; MJ0827; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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-!- SIMILARITY: BELONGS TO THE BAND 7 / MEC-2 FAMILY.
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                                                                                                                                                                                                                                                                                 VDAINQAADCWGIRCLRYEIKDIHVPPRVKESMQMQVEAERRKRATVLESEGTR 211
                                                                                                                                                                                                                                                                                                               VVKVDAVVYYRVIDVEKAILEVEDYEYAIINLAQTTLRAIIGSMELDEVLNKREYINSKL
                                                                                                                                                                                                                                                                                                                                TLQIDGVLYLRIMDPYKASYGVEDPEYAVTQLAQTTMRSELGKLSXDKVERERESLNASI 157
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67; Conser
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(Rel.
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                                                                               (Rel. 39, Created)
(Rel. 39, Last sequence update)
(Rel. 40, Last annotation update)
protein PH1511.
                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         20.1%;
                                 Thermococcales; Thermococcaceae; Pyrococcus
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                                                                                                                                                                   PRT;
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YJ33_PYRAB
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Best Local Similarity
Matches 72; Conserv
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16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y., Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y., Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K., Masuchi Y., Shizuya H., Kikuchi H.; Robb F.T., Horikoshi K., "Complete sequence and gene organization of the genome of a hyper-thermophilic archaebacterium, Pyrococcus horikoshii OT3.";
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                                              STRAIN-ORSAY;
                                                           SEQUENCE FROM
                                                                                         Archaea; Euryarchaeota; NCBI_TaxID=29292;
                                                                                                                        Pyrococcus abyssi.
                                                                                                                                          Hypothetical PAB1933.
                                                                                                                                                                                                                       YJ33_PYRAB
Q9V0Y1;
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Hypothetical protein; Transmembrane;
TRANSMEM 7 27 POTENTIL
SEQUENCE 266 AA; 2999 MW; 21D06
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InterPro; IPR001972; Stomatin.
Pfam; PF01145; Band_7; 1.
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   "Pyrococcus abyssi genome
                             Heilig R.;
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SIMILARITY: BELONGS TO THE BAND 7 / MEC-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                               NVAEGKKQAQI-----LASEAEKAEQINQAAGEASAVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NVTLQIDGVLYLRIMDPYKASYGVEDPEYAVTQLAQTTMRSELGKLSXDKVFRERESLNA 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                              NVPVRVNAVVYFRVVDPVKAVTQVKNYIMATSQISQTTLRSVIGQAHLDELLSERDKLNM 141
and
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(Rel. 40,
(Rel. 40,
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A
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33.0%;
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                                                                                                         Thermococcales;
             sequence: insights
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Pred. No. 1.5e-14;
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; '21D06F199C31021F CRC64;
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                                                                                                         Thermococcaceae;
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              archaeal chromosome
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RESULT 9
BAN7_HUMAN STANDARD; PRT; 287 AA.
ID BAN7_HUMAN STANDARD; PRT; 287 AA.
AC P27105; Q14087; Q15609;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-CCT-2001 (Rel. 40, Last annotation update)
DT 16-CT-2001 (Rel. 40, Last annotation update)
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InterPro; IPR001972; Stomatin.
Pfam; PF01145; Band_7; 1.
PRINTS; PR00721; STOMATIN.
SMART; SM00724; PHB; 1.
PROSITE; PS012470; BAND_7; 1.
PROSITE; PS01270; BAND_7; 1.
Hypothetical protein; Transmembrane; Complete Hypothetical protein; Transmembrane; Complete TRANSMEM 1 21
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band
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                                                                                          SEQUENCE FROM N.A.
MEDLINE=96423038; PubMed=8825639;
Unfried I., Entler B., Prohaska R.
                                                                                                                                                                                                                                                                                                            Stratowa
                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE-91355220; PubMed-1883838;
Hiebl-Dirschmied C.M., Entler B., Glotzmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                  Stratowa C., Prohaska R.;
"Cloning and nucleotide sequence of cDNA encoding human erythrocyte band 7 integral membrane protein.";
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                   ied I., Entler B., Prohaska R.;
organization of the gene (EPB72) encoding the
7 integral membrane protein (protein 7.2b).";
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76; Conserv
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268 AA; 30241 MW;
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1090:123-124(1991)
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Pred. No. 3.8e-14;
4; Mismatches 83
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EMBL; X60067; CAA42671.1; -
EMBL; X85116; CAA59436.1; J
EMBL; X85117; CAA59436.1; J
EMBL; W81635; AAA58432.1; -
EMBL; U33913; AAC50296.1; J
EMBL; U33925; AAC50296.1; J
EMBL; U33927; AAC50296.1; J
EMBL; U33927; AAC50296.1; J
EMBL; U33928; AAC50296.1; J
EMBL; U33929; AAC50296.1; J
EMBL; U33929; AAC50296.1; J
EMBL; U33929; AAC50296.1; J
EMBL; U33929; AAC50296.1; J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Structure, organization, and expression of the a candidate gene for hereditary hydrocytosis."; J. Biol. Chem. 270:26358-26363(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stewart G.W., Hepwort Argent A.C., Casimir Submitted (DEC-1991)
CONFLICT
                                     DOMAIN
MOD_RES
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structure.";
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Snyers L., Umlauf E., Prohaska R.;
"Cysteine 29 is the major palmitoylation site on stomatin.
FEBS Lett. 449:101-104(1999).
-I- FUNCTION: THOUGHT TO REGULATE CATION CONDUCTANCE.
-I- SUBCELLULAR LOCATION: EXPOSED ON THE CYTOPLASMIC SURFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99268434;
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SMART; SM00244; PHB;
                                                                                                                                                InterPro; IPR001972; Stomatin.
Pfam; PF01145; Band_7; 1.
PRINTS; PR00721; STOMATIN.
                                                                                                                                                                   InterPro; IFRO01972;
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"Identification of the phosphorylation site
                            LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                               European Bioinformatics Institute. There are no rest by non-profit institutions as long as its content
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DISEASE: DEFECTS IN EPB72 IN RED CELLS OF PATIENTS WITH HEREDITARY
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                                                                                                                      PS01270; BAND_7; 1.
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                                                                                                                                                                                        IPR001107; Band_7.
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549650
                                                                                                          Transmembrane;
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EXPOSED ON THE CYTOPLASMIC SURFACE
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CYTOPLASMIC
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01-NOV-1997
15-DEC-1998
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-BRISTOL N2;
Latreille P., Gattung S.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
-i- SIMILARITY: BELONGS TO THE BAND 7 / MEC-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UNC1_CAEEL Q21190;
                                                                                                                                                                                  PRINTS; PR00721; STOMATIN.
SMART; SM00244; PHB; 1.
PROSITE; PS01270; BAND_7;
                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Rhabditidae; Peloder
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                                                                                                                                                                      Transmembrane; Multigene family
                                                                                                                                                                                                                     Pfam; PF01145; Band_7;
                                                                                                                                                                                                                                  InterPro; IPR001107; Band_7.
InterPro; IPR001972; Stomatin.
                                                                                                                                                                                                                                                           WormPep;
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                                                         VPQQEAWVVERMGR--FHRILEPGLNILIPVLDRIRYVQSLKEIVINVPEQSAVTLDNVT
RAKVIAAEG----EMNASRALKEASMVITESPAALQL
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65; Conserv
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35,
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2; Mismatches
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                                                 EMBL; U50997; AAB18857.1; JOIN EMBL; U50998; AAB18857.1; JOIN MGD; MGI:95403; Epb7.2. InterPro; IPR001107; Band_7. InterPro; IPR001972; Stomatin.
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Genomics 34:410-412(1996).
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01-OCT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update
Erythrocyte band 7 integral membrane protein
7.28)
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01-OCT-1996 (Rel. 34, L
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                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no restricted the companies of the companies of the control of the companies of
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Mammalia; Eutheria;
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                 PRINTS;
                                        Pfam; PF01145; Band_7;
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                                                                                                                                                                    U50995;
U50996;
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U17297;
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                                                                                                                                                                                                              U50993;
U50994;
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7; AAA75024.1; -.
8; AAB18857.1; ALT_SEQ.
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Rodentia;
                                                            Stomatin.
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Sciurognathi;
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protein (
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thi; Muridae;
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RESULT 12
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                                                                                                                                                                                                               Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases -!- SIMILARITY: BELONGS TO THE BAND 7 / MEC-2 FAMILY.
                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                      STO-2 OR F32A6.5.
Caenorhabditis elegans.
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TRANSMEM
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                                                                              WormPep; F32A6.5; CE04473.
                                                                                         EMBL; U40409; AAA81390.1; -.
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                                                                     InterPro;
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                                                                                                                                                                                                                                                                                                                                                protein
                                                                                                                  an email to license@isb-sib.ch).
                                                       IPR001107; Band_7.
IPR001972; Stomatin
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PALMITATE (PARTIAL) (BY SIMILARITY).

V -> A (IN REF. 2).

I -> F (IN REF. 2).

L -> I (IN REF. 2).

F -> L (IN REF. 2).

V -> I (IN REF. 1).

N -> H (IN REF. 1).
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Pred. No. 2.8e-11;
0; Mismatches 79;
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PRINTS; PR00721; STOMATIN. SMART; SM00244; PHB; 1.

Pfam; PF01145; Band\_7;

InterPro;

Transmembrane;

Multigene family.

BAND\_7;

PROSITE; PS01270;

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RESULT 13
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InterPro; IPR001972; Stomatin.
Pfam; PF01145; Band_7; 1.
PRINTS; PR00721; STOMATIN.
SMART; SM00244; PHB; 1.
PROSITE; PS01270; BAND_7; 1.
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                    Transmembrane; SEQUENCE 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
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Eukaryota; Metazoa; Nen
Rhabditidae; Peloderina
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15-DEC-1998
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Local Similarity 27.5%;
nes 73; Conservative
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OR F08C6.4
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280 '
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(Rel.
               Conservative
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31000 MW;
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                                15.2%;
25.2%;
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Pred. No. 7.2e-11;
4; Mismatches 78
             Score 269; DB 1;
Pred. No. 9.7e-11;
2; Mismatches 99
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               EMBL; U26736; AAA87552.1; -. EMBL; U26735; AAA87551.1; -. EMBL; U41021; AAA82333.1; -. EMBL; U41021; AAA82333.1; -. WormPep; F14D12.4; CE04393. InterPro; IPR001107; Band_7. InterPro; IPR001972; Stomatin.
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Q27433;
Q1-NOV-1997 (Rel. 3
01-NOV-1997 (Rel. 3
01-NOV-1997 (Rel. 3
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MEDLINE-96069765; PubMed-7477350;
Huang M., Gu G., Ferguson E.L., Chalfie
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the European Bioinformatics Institute
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Band_7;
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Best Local Similarity
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                         WormPep; T04F8.5; CE18926.7.
InterPro: IPR001107; Band.7.
InterPro: IPR001972; Stomatin.
pfam; PF01145; Band.7; 1.
SMART; SM00244; PHB; 1.
                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SMART; SM00244; PHB; 1.
PROSITE; PS01270; BAND_7; 1.
                                  Transmembrane; Multigene family. NON_TER 1 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
-- I- SIMILARITY: BELONGS TO THE BAND 7 / MEC-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STO-4 protein (Fragment).
STO-4 OR T04F8.5.
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SEQUENCE 481 AA; 51899 MW;
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                                                                                            PROSITE;
                                                                                                                                                                                                                                                                    EMBL; Z66565; -; NOT_ANNOTATED_CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lennard N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EGKKQAQILASEAEKAEQINQAAGEASAVLAKAKAKAEAIRILAAALTQHNGDAAASLTV 278
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                                                                                            PS01270; BAND_7; 1.
      213 AA;
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23380 MW; D4EB210BB9D56B28 CRC64;
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; 37D2894AD39E040A CRC64;
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DA---ADVIAT 196
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                                                                                                                                                                                                VQEYERAVIFRLGRLKHGGARGPGIFFIIPCIESFKKI-DLRVVSFDVPPQEILSKDSVT
                                EGKKQAQILAS 229
                                                                 AALDEATDPWGVKVERVEIKDVRLPIQLQRAMAAEAEAARAAGAKIIAAEGEQLASRALA 188
                                                                                              DAINQAADCWGIRCLRYEIKDIHVPPRVKESMQMQVEAERRKRATVLESEGTRESAINVA 218
                                                                                                                                VSVDAVIYFRISNATVSVINVEDAARSTKLLAQTTLRNFLGTRTLAEMLSSRDAISMQMQ 128
                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                              14.0%; Score 247; DB 1; 1
28.8%; Pred. No. 1.8e-09;
28.8%; Mismatches 76;
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Search completed: September 22, 2002,  $18:3\dot{0}:47$  Job time: 545 sec

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1639
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1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
4: sp_human:*
5: sp_inverteb:
6: sp_manmal:*
7: sp_mhc:*
8: sp_organel:
9: sp_phage:*
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Maximum Match 100
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Q99JB2
Q9W1F7
Q9WVP9
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Q9YVP9
Q9T082
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Q9LVW0
G9Z1G8
Q9Z1G8
Q9Z1G8
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Q9dcg8 mus musculu
Q9w1f7 drosophila
Q9wvp9 caenorhabdi
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Q$3vp9
Q$t082
Q$1vw0
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o	OXZW6O	16	305	4	423.5	Ñ
w	Q98H59	16	316		w	ï
Q9rqu5 clostridium	Q9RQU5	Ν	320	5.	4	0
Q97k67 clostridium	Q97K67	16	322	<u>ن</u>	442.5	9
	Q9CBM5	16	374	Ģ	444.5	8
	Q92M51	16	328	5	454	7
	Q9UYE4	17	299	6.	460	5
058205 pyrococcus	058205	17	298	6	460	ű
	Q9K458	N	343	6	464.5	4
	Q9KTC6	16	306	6	467.5	ũ
Q9cmel pasteurella	Q9CME1	16	307	9	473	Ñ
Q9f507 escherichia	Q9F507	2	325	26.9	474.5	Ξ
	Q9x9Z6	2	319	5	475	ö
ס	Q9AHZ8	N	306	7.	477	9
Ω	Q9A331	16	310	7.	486	8
Q9pgw3 xylella fas	Q9PGW3	16	337	8	496.5	7
l deinococ	Q9RSI1	16	344	œ	497	6
4 m 5	Q9U4M5	ഗ	357	7.	664	Š
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=	Q9K2T7	2	315	0	711.5	Ñ
Q9jrd6 neisseria m	Q9JRD6	16	315			ï
Q9jpg5 neisseria m	д9лрс5	2	315	0		Õ
ne	Q9JPN3	N	315	0	714	છ
ph5 n	Q9JРН5	N	315	40.4	714.5	8
Q9jr80 neisseria m	Q9JR80	16	315	40.5	716	7

## ALIGNMENTS

RESULT Q9UJZ1

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Q9UJZ1
Q9UJZ1
Q9UJZ1;
Q9UJZ1;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MEMBRANE ASSOCIATED PROTEIN SLP-2 (STOMATIN-LIKE PROTEIN 2) (STOMATIN-LIKE PROTEIN 2) (STOMATIN-LIKE 2) (CDNA FLJ14499 FIS, CLONE NT2RM1000080, WEAKLY SIMILAR TO UNC-1 PROTEIN) (STOMATIN-LIKE 2).
                                                                                                                                                 "A novel member of the stomatin/EPB72/MEC-2 protein 2 (SLP2), is ubiquitously expressed chromosome 9p13.1.";
                                                                                                                                                                                                                                                                                    TISSUE=HEART MUSCLE; Wang Y., Morrow J.S.; Wang Y., Morrow J.S.; Mand Characterization of Human SLP-2, a Novel Homologue "Identification and Characterization of Human SLP-2, a Novel Homologue of Stomatin (band 7.2b) Present in Erythrocytes and Other Tissues."; Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                Owczarek C.M., Treutlein H.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                Strausberg R.;
Submitted (FEB-2001)
                                                                                                                                   Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HUSLP2 OR SLP2
                 SEQUENCE FROM N.A.
                                                                                   TISSUE-LUNG
                                                                                                   SEQUENCE FROM N.A
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[sogai T.,
Ota T.,
                                                                                  CARCINOMA,
                                                                                                                                                                                                                                                    N.A.
Hayashi K.,
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                                                                                  SKIN, AND MELANOTIC MELANOMA.;
                                                  the
                                                  EMBL/GenBank/DDBJ databases
Sugiyama T., Otsuki T., Suzuki Y.,
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plasmodium

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RESULT
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Submitted (OCT 2001) to the EMBL, BMBL; BAF190167, BAF09142.1;

EMBL; AF190167, BAF091466.1;

EMBL; BC003025, AAH03025.1;

EMBL; BC002442; BAH03025.1;

EMBL; BC002442; BAB55091.1;

EMBL; BC002449; BAB55091.1;

EMBL; BC014990; BAH14990.1;

InterPro; IPR001107; Band_7;

InterPro; IPR001107; Band_7;

InterPro; IPR001107; Stomatin.

Pfam; PF01145; Band_7; 1.

PRINTS; PR00721; STOMATIN.

SMART; SM00244; PHB; 1.

SMART; SM00244; PHB; 1.
                                                                                                                                                                                                                 Q96FY2 PRELIMINARY; PRT; 356 AA.
Q96FY2;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update stronger 11, Like 2.
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"NEDO human cDNA sequencing project.";
"Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
  Strausberg
Submitted (
                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                  TISSUE-LUNG CARCINOMA;
                                                                           SEQUENCE FROM N.A.
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                                                                                                                      NCBI_TaxID=9606;
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letazoa; Chordata;
theria; Primates;
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Pred. No. 1.2e-97;
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                                                                                                                                                  Catarrhini;
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                                               Query Match
Best Local S
Matches 330
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Best Local S
Matches 340
                                                                                                           Zhang Q.H., Ye M., Wu X.Y., Ren S.X., Zhao M., Zhao C.J., Fu G.,
A Shen Y., Fan H.Y., Lu G., Zhong M., Xu X.R., Han Z.G., Zhang J.W.,
A Tao J., Huang Q.H., Zhou J., Hu G.X., Gu J., Chen S.J., Chen Z.;
Tao J., Huang Q.H., Zhou J., Hu G.X., Gu J., Chen S.J., Chen Z.;
The coning and functional analysis of cDNAs with open reading frames for stemprogenitor cells.";
Stemprogenitor cells.";
Stemprogenitor cells.";
Genome Res. 10:1546-1560(2000).
R EMBL, AF161458; AAF29073.1;
R InterPro; IPR001107; Band_7.
R InterPro; IPR001107; Band_7.
R InterPro; IPR001107; STOMATIN.
R Pfam; PF01145; Band_7; 1.
R Pfam; PF01145; Band_7; 1.
R SMART; SM00244; PHB; 1.
R SMART; SM00244; PHB; 1.
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Q9P042;
01-OCT-2000
01-OCT-2000
01-DEC-2001
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Mammalia; Eutheria;
NCBI_TaxID=9606;
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nilarity 97.1%;
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                                               Score 1613.5; DB Pred. No. 1.4e-95; 3; Mismatches 4
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Pred. No. 3.4e-97;
2; Mismatches 12
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TISSUE-FIBROBLAST OR FORESKIN;

TISSUE-FIBROBLAST OR FORESKIN;

Lamerdin J.E., McCready P.M., Skowronski E., Adamson A.W.,

Lamerdin J.E., McCready P.M., Kyle A., Ramirez M., Stilwagen S.,

Burkhart-Schultz K., Gordon L., Kyle A., Ramirez M., Stilwagen S.,

Phan H., Velasco N., Garnes J., Danganan L., Poundstone P.,

Christensen M., Georgescu A., Avila J., Liu S., Attix C., Andreise

Trankheim M., Amico-Keller G., Coefield J., Duarte S., Lucas S.,

Bruce R., Thomas P., Quan G., Kronmiller B., Arellano A.,

Montgomery M., Ow D., Nolan M., Trong S., Kobayashi A., Olsen A.O.,

Carrago A.V., Ow D., Nolan M., Trong S., Kobayashi A., Olsen A.O.,
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Mammalia; Eutheria;
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93
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InterPro; IPR001972; Stomatin.
Pfam; PF01145; Band_7; 1.
PRINTS; PR00721; STOMATIN.
SMART; SM00244; PHB; 1.
SEQUENCE 353 AA; 38385 MW;
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Q99JB2;
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EMBL; BC003425; AAG53404.1; -
EMBL; AF323178; AAG53404.1; -
EMBL; MGI:1913842; 0610038F01Rik.
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                                                                                                                                                                                                                                                                                                                                                                PSNPGDVTSMVAQAMGVYGALTKAPVPGTPDSLSSGSSRDVQGTDASXDEELDRVKMS 356
                                                                                                               QAAGEASAVLAKAKAKAEAIRILAAALTQHNGDAAASLTVAEQYVSAFSKLAKDSNTILL
                                                                                                                                                                                                                                                                                                    VEDPEYAVTQLAQTTMRSELGKLSXDKVFRERESLNASIVDAINQAADCWGIRCLRYEIK 178
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                                                                                         QAAGEASAVLAKAKAKAEAIRILAGALTQHNGDAAASLTVAEQYVSAFSKLAKDSNTVLL
                                                                                                                                                                                  DIHVPPRVKESMOMQVEAERRKRATVLESEGTRESAINVAEGKKOAQILASEAEKAEQIN
                                                                                                                                                                                                                                                                           VEDPEYAVTQLAQTTMRSELGKLSLDKVFRERESLNANIVDAINQAADCWGIRCLRYEIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 89.9
22; Conservative
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IS (Mouse).
Metazoa; Chordata; C
Metazoa; Rodentia; C
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(TrEMBLrel. 17, Last sequence up
(TrEMBLrel. 19, Last annotation
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89.9%;
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Pred. No. 1e-90;
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Sciurognathi; Muridae;
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353
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RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
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RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schrini L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Toyo-oka K., Wang K. H., Weltz C., Whittaker C., Wilming L.,
RA Mynahaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 320;
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InterPro; IPR001972; Stomatin.
Pfam; PF01145; Band_7; 1.
PRINTS; PR00771; STOMATIN.
SMART; SM00244; PHB; 1.
SEQUENCE 353 AA; 38530 MW; I
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Q9DCG8;
01-JUN-2001
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EMBL; AK002793; BAB22363.1; -.
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MEDLINE-21085660;
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01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
0610038F01RIK PROTEIN.
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                                                                          VEDPEYAVTQLAQTTMRSELGKLSXDKVFRERESLNASIVDAINQAADCWGIRCLRYEIK 178
                                                                                                                                                                                                                                                                                                                                                                                                           PSNPGDVTSMVAQAMGVYGALTKAPVPGTPDSLSSGSSRDVQGTDASXDEELDRVKMS
                                                                                                                                                                                                                     DIHVPPRVKESMOMQVEAERRKRATVLESEGTRESAINVAEGKKQAQILASEAEKAEQIN
                                                                                                                                                                                                                                                                                                        VEDPEYAVTQLAQTTMRSELGKLSLDKVFREREFLNANIVDAINQAADCWGIRCLRYEIK
                                                                                                                                                                                           DIHVPPRVKESMQMQVEAERRKRATVLESEGTRESAINVAEGKKQAQILASEAEKAEQIN
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6J; TISSUE-KIDNEY;
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Last annotation updat
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Pred. No. 5.2
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RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.
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RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson K.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Spier E., Spradling A.C., Stapheton M., Strong R., Sun E.,
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RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
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Pacence 287:2185-2195(2001).
DR EMBL, AE003462; AARA/110.1:
DR InterPro; IPR0011972; Stomatin
DR InterPro; IPR0011972; Stomatin
DR InterPro; IPR0011972; Stomatin
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Q9W1F7;
Q1-MAY-2000
Q1-MAY-2000
Q1-JUN-2001
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Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
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Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn I
Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann I
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
PRINTS; PR00721; STOI
SMART; SM00244; PHB;
SEQUENCE 323 AA;
                                                                       InterPro; IPR001972; Stomatin
Pfam; PF01145; Band_7; 1.
PRINTS; PR00721; STOMATIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               eoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Drosophilidae; Drosophila.
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       35668 MW;
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Last annotation updat
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          D5C6241445FEF4DE CRC64
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Query Match Best Local Similarity

60.2%;

Score 1064.5; DB Pred. No. 1.6e-60;

DB 5;

Length

17;

Gaps

2

209;

Conservative

55;

Mismatches

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                                                                                                                                                Query Match 54.2%; Score 957.5;
Best Local Similarity 61.2%; Pred. No. 1.1
Matches 188; Conservative 58; Mismatches
                                                                                                                                                                                                            investigating biology.";
Sclence 282:2012-2018(1998).
EMBL; Z81072; CABO3018.1; -
InterPro; IPR001107; Band_7.
InterPro; IPR001972; Stomatin.
Pfam; PF01145; Band_7; I.
PRINTS; PR00721; STOMATIN.
SMART; SM00244; PHB; I.
SEQUENCE 334 AA; 36704 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9XVP9 PRELIMINARY; PRT; 334 AA.
Q9XVP9;
Q1-NOV-1999 (TrEMBLrel. 12, Created)
Q1-NOV-1999 (TrEMBLrel. 12, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
F30A10.5 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99069613;
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                           Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                           "Genome sequence of the nematode
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           MRSELGKLSXDKVERERESLNASIVDAINQAADCWGIRCLRYEIKDIHVPPRVKESMQMQ 193
                                                                                             STLPLAVTSSROAHAAHNTVINFVPQQEAWYVERMGKFYKILEPGLNFLLPIIDKIKFV 83
                                                                                                           SSGLP-----RNTVVLEVPQQEAWVVERMGREHRILEPGLNILIPVLDRIRYV 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AEQYIGAFKKLAKTNNTMILPSNPGDVNGFVAQALAVYNHVSNS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AEQYVSAFSKLAKDSNTILLPSNPGDVTSMVAQAMGVYGALTKAPVPGTPDSLSSGSSRD 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EGKKQAQILASEAEKAEQINQAAGEASAVLAKAKAKAEAIRILAAALTQHNGDAAASLTV 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DSINKASEAWGIACLRYEIRDIRLPTRVHEAMQMQVEAERRKRAAILESEGVREAEINIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LQIDGVLYLRIMDPYKASYGVEDPEYAVTQLAQTTMRSELGKLSXDKVFRERESLNASIV 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MFVPQQEAWVVERMGRFHRILDPGLNILVPVADKIKYVQSLKEIAIDVPKQSAITSDNVT
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MRSEVGKINLDTVFKERELLNENIVFAINKASAPWGIQCMRYEIRDMQMPSKIQEAMQMQ
                                               QNLREIAIEIPEQGAITIDNVQLRLDGVLYLRVFDPYKACDASYGVDDPEFAVTQLAQTT 143
                                                                                                                                                                                                                                                                                                                                                                                          (OCT-1996)
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Best Local Similarity
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O60121;
01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PYPOTHETICAL 39.3 KDA PROTEIN C16G5.07C IN CHROMOSOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; iPR001107; Band_7.
InterPro; iPR001972; Stomatin.
Pfam; PF01145; Band_7; 1.
SMART; SM00244; PHB; 1.
PROSITE; PS01270; BAND_7; FALSE_NEG
Q93VP9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
SEQUENCE 354 AA; 39274 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (MAY-1998) to the EMBL/GenBank/DDBJ -:- SIMILARITY: BELONGS TO THE BAND 7 / MEC-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schizosaccharomyces pombe (Fission yeast).
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Reinhardt R
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                                                                                                                                                                                                               INVAEGDKQAEILDSEGQKIKTINSALAEAQAIREKASATASGIAVLADSIKKQEHGLEA
                                                                                                                                                                                                                                             INVAEGKKQAQILASEAEKAEQINQAAGEASAVLAKAKAKAEAIRILAAAL-TQHNGDAA
                                                                                                                                                                                                                                                                                                           IHITDAINKAAESWGIRCLRHEIRDIRPPESYVMAMHQQVSAERQKRAEILESEGKRQAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NTIIKFVPQQVAYVVERMGRFSRILTPGVAFLAPIIDKIAYIHSLKERALEIPTQSAITL
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PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56;
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  PRT;
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Best Local S
Matches 168
  Q9T082;
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EMBL; AY059109; AAL15215.1; -.
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Yamada K., Banh J., Banno F., Chang E., Dale J.M., Goldsmith A.D.,

Yamada K., Banh J., Banno F., Chang C., Toriumi M., Wu H.C.,

Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Wu H.C.,

Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Cheuk R.,

Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin Neumann G.,

Kawai J., Kim C., Koesema E., Lam B., Lin J., Meyers M.C., Miranda M.,

Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M.,

Shinn P., Southwick A., Tracy S.E., Shinozaki K., Davis R.W.,
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence up
01-DEC-2001 (TrEMBLrel. 19, Last annotation
HYPOTHETICAL 45.0 KDA PROTEIN.
AT4G27580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ecker J.R., Theologis A.; "Full Length cDNA of gene AT4g27580 (GI:7269612)."; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ datab
                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein. SEQUENCE 411 AA; 4
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                                                                                               TKAPVPGTPDSLSSGSSRDVQGTDASXDEELDRVK 354
                                                                                                             ILAAALTQHNGDAAASLTVAEQYVSAFSKLAKDSNTILLPSNPGDVTSMVAQAMGVYGAL 319
                                                                                                                                                                         KRAQILESEGERQSHINIADGKKSSVILASEAAKMDQVNRAQGEAEAILARAQATAKGLV
                                                                                                                                                                                    KRATVLESEGTRESAINVAEGKKQAQILASEAEKAEQINQAAGEASAVLAKAKAKAEAIR
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                                                                                                                                                                                                                                                                                                                     SSGLPRNTVVL-----FVPQQEAWVVERMGREHRILEPGLNILIPVLDRIRYVQSL 79
                                                                                                                                                                                                                                                                                                                                                                       168;
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               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                46.78;
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Pred. No. 3.8e
57; Mismatches
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               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                          Length 411;
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Q9LVW0;
Q9LVW0;
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RESULT
Q9LVW0
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Best Local Similarity
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EMBL; AL161571; CAB81408.1; ---
InterPro; IPR001107; Band_7.
InterPro; IPR001972; Stomatin.
Pfam; PF01145; Band_7; 1.
PRINTS; PR00721; STOMATIN.
SWART; SM00244; PHB; 1.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 55.9 KDA PROTEIN.
T29A15.70 OR AT4G27580.
Arabidopsis thallana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatcophyta; Magnollophyta; eudicotyledons; core eudicots; Rosid
eurosids II, Brassicales; Brassicaceae; Arabidopsis.
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Bevan M., Van Der Schueren
Volckaert G., Hoheisel J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein SEQUENCE 515 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted
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                   12
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                                                                                                       TKAPVPGTPDSLSSGSSRDVQGTDASXDEELDRVK
                                                                                                                                        LLSQSLKETGGVEAASLRVAEQYITAFGNIAKEGTIMLLPSGASNPASMIAQALTMYKSL
                                                                                                                                                                                                                            KRATVLESEGTRESAINVAEGKKQAQILASEAEKAEQINQAAGEASAVLAKAKAKAEAIR
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(MAR-1999) to the EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 826; DB 10;
; Pred. No. 5.1e-45;
67; Mismatches 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J., Chuang Y-J., Voet M., Rot
Mewes H.W., Mayer K.F.X., Scl
e EMBL/GenBank/DDBJ databases
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Schueller
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Best Local Similarity
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clones.";
clones. 7:31-63(2000)
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
            Ogata H., Audic S., Samson D., Roux V., Raoult D.;
                                           MEDLINE=21442074; PubMed=11557893;
                                                             SEQUENCE FROM N.A. STRAIN=MALISH 7;
                                                                                              Bacteria; Proteobacteria; alp Rickettsiaceae; Rickettsieae; NCBI_TaxID=781;
                                                                                                                                                HYPOTHETICAL PROTEIN RC0452 RC0452.
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01-DEC-2001
                                                                                                                                                                                                                          Q92IG8
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SMART; SM00244; PHB; 1.
SEQUENCE 401 AA; 43607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AB018115; BAA97132.1; Interpro: IPR001107; Band_7. Interpro: IPR001972; Stomatin. Pfam; PF01145; Band_7; 1.
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01-JUN-2001 (TrEMBLrel 17, Last annotation update)
SIMILARITY TO STOMATIN LIKE PROTEIN.
Arabidopsis thaliana (Mouse-ear cress).
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                                                                                                                                    Rickettsia conorii.
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 Mechanisms
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1-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 TLDNVTLQIDGVLYLRIMDPYKASYGVEDPEYAVTQLAQTTMRSELGKLSXDKVFRERES 152
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Nakamura Y., Kaneko T., Katoh T., Asamizu
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55.1%; Pred. No. 1.5e-44;
tive 58; Mismatches 72
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Matches 158; Conser
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Nature 396:133-140(1998).
EMBL; AJ235271; CAA14788.1; -.
InterPro; IPR001107; Band 7.
InterPro; IPR001972; Stomatin.
Pfam; PF01145; Band 7; 1.
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Q9ZDKO;
Q1-MAY-1999
Q1-MAY-1999
Q1-DEC-2001
                                                                                                                                          PRINTS; PRO0721; STOMATIN.
SMART; SM00244; PHB; 1.
Hypothetical protein; Complete
SEQUENCE 311 AA; 34040 MW;
                                                                                                                                                                                                                                                                    MEDLINE=99039499; PubMed=9823893;
Andersson S.G.E., Zomorodipour A., Andersson J.O.,
Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M.,
Eriksson A.-S., Winkler H.H., Kurland C.G.;
"The genome sequence of Rickettsia prowazekii and th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein; Complete proteome. SEQUENCE 312 AA; 34025 MW; A41878CAAABC49F5 CRC64;
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EMBL; AE008609; AAL02990.1; -
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VTLQIDGVLYLRIMDPYKASYGVEDPEYAVTQLAQTTMRSELGKLSXDKVFRERESLNAS
                         MVKVVPQQQAWVVEKLGKFDKVLQPGLNLLIPIIQRVAYKHTLKEEAIDVTAQTAISNDN
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"Prohibitins, Stomatins, and Plant Disease Response Genes Com

Trotein Superfamily that Controls Cell Proliferation, Ion Cha

Regulation, and Death.";

L. Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.

R EMBL; AF236372; AAF68388.1; -.

R InterPro; IPR001107; Bandd_7.

R InterPro; IPR001972; Stomatin.

R Pfam; PF01145; Bandd_7; 1.

R Pfam; PF01145; Bandd_7; 1.

R Pfam; PF01145; Bandd_7; 1.

R Pfam; SM00244; PHB; 1.

SMART; SM00244; PHB; 1.

SMART; SM00244; PHB; 1.
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Q9M585;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
STOMATIN-LIKE PROTEIN.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
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328 FVAQAMKTYEQIHSHSQALKSHPQIEELKESGETSPAPSSEASKTPPLIEEADSNQTFSL
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                                                                               308 MVAQAMGVY-----GALTKAP------VPGTPDSLSSGSSRDVQGTDASXDEEL 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QAMEMQAEAERKKRAQILESEGMKQAQILESEGKKTAQILESEGAMLDLANRAKGAAEAI 267
                                                                                                                                                                                                                                                                                        ESMQMQVEAERRKRATVLESEGTRESAINVAEGKKQAQILASEAEKAEQINQAAGEASAV 247
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Db 388 QRPK 391

Search completed: September 22, 2002, 18:30:03 Job time: 546 sec

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; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBanl
; CLONE: 1353669
US-08-781-562-5
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                                                                                 Query Match
Best Local
                                                            Matches
                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 415 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/781,562
FILING DATE: Herewith
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: NOVEL HUMAN MEMBRANE PROTEIN NUMBER OF SEQUENCES: 7
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APPLICANT: Goli, Surya K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 TSVDAVIYYRISNATVSVANVENAHHSTRLLAQTTLRNMLGTRSLSEILSDRETLAASMQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 3174 POI
CITY: Palo Alto
STATE: CA
40 FVPQQEAMVVERMGRFHRILEPGLNILIPVLDRIRYVQSLKEIVINVPEQSAVTLDNVTL 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 VQEYERAVIFRIGRLIGGGAKGPGIFFVLPCIESYTKV-DLRTVSFSVPPQEILTKDSVT 120
                                                                               Local
                                                                                                                                                                                                                                                              STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --RYLQTLNSVAREKFDDHLPTSDG 278
                                                          tch 9.6%; Score 169; DB 1; I al Similarity 23.1%; Pred. No. 2.2e-08; 61; Conservative 53; Mismatches 120;
                                                                                                                                                                                                                                                                                   amino acid
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; MOLECULE TYPE:
US-08-279-270A-1
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Best Local Similarity
Watches 73; Conserv
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INFORMATION FOR SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: Concurrently
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mayfield, Denise L.
REGISTRATION NUMBER: 33,7
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS: LENGTH: 379 amino acids
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                                      144 DKVFRERESLNASIVDAINQAADCWGIRCLRYEIKDIH-------------
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ZIP: 77210
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  72
                                                                         12 TAEGVALTVTGVAQVKIMTEKELLAVACEQFLGLNVQDIKNVVLQTLEGHLRSILGTLTV
                                                                                                     93 TLDNVTLQIDGVLYLRIMDPYK------ASYGVEDPEYAVTQLAQTTMRSELGKLSX 143
                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DÓCKET NUMBER:
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EQIYQDRDQFAKLVREVAAPDVGRMGIEILSFTIKDVYDKVDYLSSLGKTQTAVVQRDAD 131
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O. Box 4433
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                                                                                                                                                      8.7%; Score 154; DB 1;
19.6%; Pred. No. 5.6e-07;
tive 54; Mismatches 108
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ER: UTSH:173--1/MAY
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US-08-781-562-3
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; LIBRARY: GenBank
; CLONE: 1591514
US-08-781-562-7
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/08781562 Patent No. 5763589
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APPLICANT: Hillman, Jennifer L.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN MEMBRANE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                        TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 530 PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/781,562 FILING DATE: Herewith
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MEDIUM TYPE: Diskett
                                                                                                                  TOPOLOGY: line
IMMEDIATE SOURCE:
                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   158 VDAINQAADCWGIRCLRYEIKDIHVPPRVKESMQMQVEAERRKRATVLESEGTR 211
                                                                        LIBRARY: GELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM CON OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 3174 POI
                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                         TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38 VLFVPQQEAWVVERMGRFHRILEPGLNILIPVLDRIRYVQSLKEIVINVPEQSAVTLDNV 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                     ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VVKVDAVVYYRVIDVEKAILEVEDYEYAIINLAQTTLRAIIGSMELDEVLNKREYINSKL 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TLQIDGVLYLRIMDPYKASYGVEDPEYAVTQLAQTTMRSELGKLSXDKVFRERESLNASI 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IVIVNQYEGGLIFRLGRVIGKLKPGINIIIPFLD-VPVKVDMRTRVTDIPPQEMITKDNA 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20.1%; Score 354.5; DB 1; al Similarity 38.5%; Pred. No. 3.9e-27; 67; Conservative 46; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94304
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                                                                                                                                                                                 288 amino acids
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                                                                                                  Genbank
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15.9%;
30.0%;
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Pred. No. 1e-19;
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                 Length 288;
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                                                                                                                                                        ; CLONE: US-08-781-562-4
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US-08-781-562-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B
                                                        Query Match 15.3%; Score 271; DB 1; I Best Local Similarity 27.5%; Pred. No. 1.1e-18; Matches 73; Conservative 64; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No. 5763589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/08781562
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: GOLL, Surya K.
                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOTTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 280 amino acids
                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: NOVEL HUMAN MEMBRANE PROTEIN NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                 IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            218 RAKVIAAEG----EMNASRALKEASMVITESPAALQL 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       158 KNLSQILSDREETAHNMQSTLDDATDAWGIKVERVEIKDVKLPVQLQRAMAAEAEASREA 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            141 LSXDKVFRERESLNASIVDAINQAADCWGIRCLRYEIKDIHVPPRVKESMQMQVEAERRK 200
41 VPQQEAWVVERMGRE--HRILEPGLNILIPVLDRIRYVQSLKEIVINVPEQSAVTLDNVT 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 3174 POI CITY: Palo Alto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/781,562 FILING DATE: Herewith
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98 TISFDIPPQEILTKDSVTISVDGVVYYRVQNATLAVANITNADSATRLLAQTTLRNVLGT 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42 TVITEPISIWMCIKIIKEYERAIIFRLG---RILQGGAKGPGLFFILPCTDSFIKV-DMR 97
                                                                                                                                                                        LIBRARY: GenBank CLONE: 1065452
                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                      STRANDEDNESS:
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                                                        Indels 50;
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; CLONE: ...
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                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION RUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEPHAX: 415-845-4166
                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 381 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Hillman, Jenniter L.
APPLICANT: GGli, Surya K.
TITLE OF INVENTION: MOVEL HUMAN MEMBRANE PROTEIN
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast-SEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                              FILING DATE: Herewit
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
               IMMEDIATE SOURCE:
LIBRARY: Owl
CLONE: 79701
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                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US
FILING DATE: Herewith
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
                                                              STRANDEDNESS:
TOPOLOGY: lir
                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MLARAARGHWGPFAEGLSTGFWPRSGRASSGLPRNTVVLFVPQQEAWVVEFMGREHRILE 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CA
                                                                                                              381 amino acids
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                                                              linear
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RESULT 3
US-08-781-562-7
; Sequence 7, Application US/08781562
; Patent No. 5763589
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Best Local Similarity
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                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,562
FILING DATE: Herewith
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                     REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hillman, APPLICANT: Goli, Sur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                323 EPSPVEDQPKHAADGDDAEVAGWFSTDTDPS 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: UZIP: 94304
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TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98 TLQIDGVLYLRIMDPYKASYGVEDPEYAVTQLAQTTMRSELGKLSXDKVFRERESLNASI 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26 VALIPQAEAAVIERLGRYSRTVSGQLTLLVPFIDRVRARVDLRERVVSFPPQPVITEDNL 85
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                                     TYPE: amino acid
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                                                     199 amino acids
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Pred. No. 2.9e-38;
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Run

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Title: Perfect score:

Scoring table: Sequence:

Minimum DB seq Maximum DB seq

Database

Result

Score

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Score 1763; DB 1; Pred. No. 2.6e-165;

Length 356;

354.5 281.5 271 169 104.5 104.5 104.5 104.5 104.5 99.5 99.5 99.5 99.5 99.5 99.5 99.5

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OM protein - protein search, using sw model
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US-08-938-30-9
US-08-938-30-9
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IMMEDIATE SOURCE:
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ZIP: 943
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CITY: Palo Alto
STATE: CA
                                                                                                         LIBRARY: Consensus CLONE: Consensus
                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: sir
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                                                                                                                                                                                                                                      LENGTH:
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ALIGNMENTS

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Sequence 1, Application US/08781562 Patent No. 5763589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Hilman, Jennifer L.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN MEMBRANE PROTEIN
NUMBER OF SEQUENCES: 7
                                                                                                                                              CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: PF-0181 US
                   TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRISTENCY DOTS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,562
                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Incyte ....
356 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Incyte Pharmaceuticals, Inc
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990S-0139453
990S-0139453
990S-0139453
990S-0139453
990S-0139453
990S-0139453
990S-0139453
   99US-0125788.
99US-0126264.
99US-0126785.
99US-0127462.
99US-0128234.
   99US-0121825
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294 vkgvgaclnaksveykelgedkssvkmn

356 321

339

VQGTDA-----SXDEELDRVKMS

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RESULT :
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  В
  δõ
  cc determining the presence of or predisposition to a disease associated cowith altered levels of polypeptide. The polypeptides are also useful for cidentifying agents (agonists and antiagonists) that bind to them. Cells cexpressing the proteins are useful for identifying a therapeutic agent (for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising cc the nucleic acids encoding the polypeptides and cells genetically criminessed to express them are also useful for producing the proteins. Cc The proteins are useful in genetic vaccination, testing and cc therapy, and can be used as nutritional supplements. They may be used to immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid cc sequences of novel human secreted proteins of the invention.
   Query Match
Best Local
  Matches
  Claim
   Tang
   Nucleic acids encoding a vaccination, testing and
   18-APR-2000; 2000US-0552929
26-JAN-2001; 2001US-0770160
  25-OCT-2001
   WO200179449-A2
  Homo sapiens
   Human; vaccination; gene therapy; nutritional supplement;
stem cell proliferation; haematopoiesis; nerve tissue regeneration;
   Novel human secreted protein #3649
  18-DEC-2001
   AAU33158;
  AAU33158 standard; Protein;
   (HYSE-)
   16-APR-2001; 2001WO-US08656
  immune
   Sequence
   Local Similarity
   10
                59
  -
   1 MLARAARGHWGPFAEG--LSTGFWPRSGRASSGLPRNTVVLFVPQQEAWVVERMGRFHRI 58
   invention relates to novel human secreted polypeptides. The ypeptides and antibodies to the polypeptides are useful for
  YT,
   2001-611725/70
  LEPGLNILIPVLDRIRYVQSLKEIVINVPEQSAVTLDNVTLQIDGVLYLRIMDPYKASYG
  20; Page 716; 765pp; English
suppression;
   HYSEQ INC.
   Liu C,
   222
  Conservative
  (first entry)
   ξ,
  Drmanac
  immune stimulation; anti-inflammatory;
   57.2%;
92.9%;
   range of human polypeptides, useful in genetic therapy – \ensuremath{^{\circ}}
  222
  2
   Score 1011; DB 22; Pred. No. 1.1e-80;
  Ã
  Mismatches
  10;
   Length
   222;
   leukaemia.
  Gaps
   58
                118
   for
   ç
  2
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AAU28241
  Вþ
   δÃ
  В
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ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy; transgenic animal; Alzheimer's disease; Parkinson's disease; burn; amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia; ulcer; osteoporosis; bone degenerative disorder; periodontal disease; gut protection; lung; liver fibrosis; immune deficiency; infection; severe combined immunodeficiency; SCID; autoimmune disorder; allergy;
           The invention relates to novel isolated human secreted polypeptides (I) and polynucleotides (II). (I) and (II) are useful for treating inflammatory conditions such as arthritis, nephritis, Crohn's disease, ischaemia-reperfusion injury, shock, sepsis, immune responses, and is involved in increasing haematopolesis, stem cell survival, bone growth and remodeling. (I), (II) and modulators of (II) are useful for prophylaxis or treatment of one or more cancers. (II) is also useful for creating transgenic animals useful for studying the in vivo activities of the polypeptide as well as for studying modulators of the polypeptides. (I) induces the proliferation of neural cells and regeneration of nerve and brain tissue and is useful for the treatment of central and peripheral nervous system diseases and neuropathies, such as Alzheimer's,
   severe combined immunodeficiency; SCID; autoimmune disorder; multiple sclerosis; rheumatoid arthritis; diabetes mellitus;
   Human; secreted protein; arthritis; Crohn's disease;
  Novel human secretory protein,
   18-DEC-2001
   AAU28241 standard; Protein; 463
   Tang
   07-MAR-2000;
  05-MAR-2001;
   13-SEP-2001.
  WO200166689-A2
  Homo sapiens.
   Novel polypeptides and nucleic acids obtained from cDNA libraries prepared from various human tissues, for diagnosis and treatment of
  N-PSDB; AAS45141.
   WPI; 2001-589934/66.
  Zhao
   19-SEP-2000;
20-OCT-2000;
   fertility; analgesic; pain; antigen.
   179
  cancer, neurological, inflammatory, and autoimmune disorders
   (HYSE-) HYSEQ INC
  19-MAY-2000;
17-JUN-2000;
   179
  119
   119
   L4-JUL-2000;
  59
  dihvpprvkesmqmqveaerrkratvlesegtresainvaegkk 222
  DIHVPPRVKESMQMQVEAERRKRATVLESEGTRESAINVAEGKK
  YT,
  lepglnilipvldriryvqslkeivinvpeqsavtldnvtlqidgvlylrimdpykasyg
  2
  Liu C,
Yang Y,
  SEQ ID
   2000US-0519705.
2000US-0574454.
2000US-0596193.
2000US-0616847.
2000US-0665363.
2000US-0693267.
   (first entry)
  2001WO-US04942
  Asundi V,
Drmanac F
   No 598; 107pp; English.
Huntington's
  RT,
  Xu C, Wehrman T, T, Zhang J, Chen
  Seq ID No
    disease,
   598.
  70
  Ren
  222
  xue
   sepsis;
  sepsis; shock;
neuropathy;
  ма
АJ,
  Y, Zhou
Wang J;
  asthma;
   118
  P
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RESULT
ABB59541
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  В
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   В
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   ş
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   QY
  밁
   В
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   Matches
   12-SEP-1997
12-SEP-1997
12-SEP-1997
02-OCT-1997
02-OCT-1997
02-OCT-1997
02-OCT-1997
02-OCT-1997
   This sequence represents a fragment of a secreted human protein encoded by the nucleic acid molecule detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Fc portion (e.g. AAX04302) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to 86 novel genes and their fragments (nucleic acid sequences: AAX04311-X04410; maino acid sequences AAW04311-X04410; which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 86 polynucleotides, based on which tissues they are most highly expressed (see AAX04311 for described research).
   Sequence
   disorders, immune diseases,
  useful
   Ľ
   (HUMA-) HUMAN GENOME SCI INC
                                      301
   351
   181
   231
  121
  171
   111
   61
  51
   Local Similarity
   isolated human genes and the secreted polypeptides they encode ful for diagnosis and treatment of e.g. cancers, neurological orders, immune diseases, inflammation or blood disorders
   RMGRFHRILEPGLNILIPVLDRIRYVQSLKEIVINVPEQSAVTLDNVTLQIDGVLYLRIM 110
                                     drvkms
  DRVKMS 356
  RCLRYEIKDIHVPPRVKESMQMQVEAERRKRATVLESEGTRESAINVAEGKKQAQILASE
   DPYKASYGVEDPEYAVTQLAQTTMRSELGKLSXDKVFRERESLNASIVDAINQAADCWGI 170
   rmgrfhrilepglnilipvldriryvqslkeivinvpeqsavtldnvtlqidgvlylrim
   KDSNTILLPSNPGDVTSMVAQAMGVYGALTKAPVPGTPDSLSSGSSRDVQGTDASXDEEL
  rclryeikdihvpprvkesmqmqveaerrkratvlesegtresainvaegkkqaqilase
  dpykasygvedpeyavtqlaqttmrselgklsldkvfrereslnasivdainqaadcwgi
  AAX04311 for described uses).
   PΑ,
   LA,
   Z
   306
                                     306
  Page
  Ebner
Ni J,
  Conservative
  97US-0060834.
97US-0060841.
97US-0060844.
97US-0060865.
97US-0061059.
   97US-0058971.
97US-0058972.
97US-0058975.
   Ą
   R, Fe
Olsen
  84.5%;
99.3%;
  Ferrie
en HS,
  English
   0
   Score 1493; DB 20;
Pred. No. 9.4e-123;
   AM, I
Rosen
  Mismatches
   Feng
n CA,
  P, Greene
Ruben SM,
  JM,
Shi
  Length
   Indels
  Lafleur DW;
Y, Young P;
  0;
   to a
  Gaps
  encoded
  300
   290
   120
   350
  180
   60
   1n
  in
  0;
             Ş
   QΥ
  В
  S
  DЪ
   Q
   DЪ
   Query Match
Best Local
   Venter
                279
                                   181
  219
   121
  159
   61
   99
  39
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Matches 209;
  The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLIG1840-ABL16175) and the encoded proteins
  The sequence data for this patent did not form specification, but was obtained in electronic fat ftp.wlpo.int/pub/published_pct_sequences.
   sequences (ABL01840 (ABB57737-ABB72072)
   Disclosure; SEQ
  New isolated nucleic a
genes from Drosophila
interactions -
   23-MAR-2000;
11-JUL-2000;
   Sequence
  23-MAR-2001;
  WO200171042-A2
   Drosophila melanogaster.
  pharmaceutical.
  Drosophila;
   Drosophila
  (PEKE ) PE
  26-MAR-2002
  ABB59541 standard; Protein;
      241
aeqyigafkklaktnntmilpsnpgdvngfvaqalavynhvsns----
  LQIDGVLYLRIMDPYKASYGVEDPEYAVTQLAQTTMRSELGKLSXDKVFRERESLNASIV 158
  LFVPQQEAWVVERMGRFHRILEPGLNILIPVLDRIRYVQSLKEIVINVPEQSAVTLDNVT
  EGKKQAQILASEAEKAEQINQAAGEASAVLAKAKAKAEAIRILAAALTQHNGDAAASLTV
  DAINQAADCWGIRCLRYEIKDIHVPPRVKESMQMQVEAERRKRATVLESEGTRESAINVA
   \verb|mfvpqqeawvvermgrfhrildpglnilvpvadkikyvqslkeiaidvpkqsaitsdnvt|
  2001-656860/75.
DB; ABL03644.
   AEQYVSAFSKLAKDSNTILLPSNPGDVTSMVAQAMGVYGALTKAPVPGTPDSLSSGSSRD
  dsinkaseawgiaclryeirdirlptrvheamqmqveaerrkraailesegvreaeinia
  {\tt lsidgvlylriidpykasygvedpefaitglaqttmrselgkmsmdkvfrereslnvsiv}
  egkrksrilaseaerqehinkasgeaaaiiavadararsllaiakslshldgqnaasltl
   JC,
   Similarity
  CORP NY.
   323
   melanogaster polypeptide SEQ ID
   Conservative
   Adams
  developmental biology; cell signalling; insecticide;
  (first entry)
   2000US-191637P.
2000US-0614150.
  2001WO-US09231
   ID NO
   ĭ
   60.2%; Score 1064.5; DB 63.7%; Pred. No. 3.9e-85;
   acid
a and
   5415;
   PWD,
   detection reager for elucidating
   55;
   21pp + Sequence Listing; English
   Myers
   Mismatches
  ΑA
   reagent for detecting 
dating cell signalling
   EW;
   Ö
   47; Indels
   5415
  o part of the printed format directly from
  22;
  Length
   1000
and c
   cell-cell
   Gaps
   338
   278
   218
   60
  240
  180
  98
    293
   120
  WIPO
  is
   ν,
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RESULT
AAM78566
  밁
 Query Match
Best Local S
Matches 341
  vaccine; pentine;
   03-FEB-2000;
27-APR-2000;
20-JUN-2000;
19-JUL-2000;
  01-SEP-2000;
15-SEP-2000;
20-OCT-2000;
  The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity, inhibin activity and may be useful in the diagnosis and/or
   Sequence
   Note: Records for SEQ ID NO 2110 (AAK52581), (AAM80020) are omitted as the relevant pages were missing at the time of publication.
  Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy -
  Xue
  (HYSE-)
  05-FEB-2001; 2001WO-US04098
   09-AUG-2001.
   WO200157190-A2
   nervous
   Human protein
   06-NOV-2001
  AAM78566
   treatment of cancer, leukaemia, nervous system disorders, arthritis and
   , AJ,
  7
  2001-476283/51.
 al Similarity
341; Conser
   cytokine; cell proliferation; cell differentiation; gene the; peptide therapp; stem cell growth factor; haematopoiesis; growth factor; immunomodulatory; cancer; leukaemia; s system disorder; arthritis; inflammation.
  HYSEQ INC.
  Liu C,
Wang D,
Yang Y,
  standard;
   Page 3486-3487; 6221pp; English.
  358
   2000US-0496914
2000US-0560875
2000US-0598075
2000US-0620325
2000US-0654936
2000US-06533561
2000US-0693325
2000US-0728422
   (first entry)
   SEQ
   Ā
  Drmanac RT, Asundi V,
Wang J, Zhang J, Ren
Wejhrman T, Goodrich R;
   ID NO 1228
  Protein; 358
           92.5%;
Score 1635; DB 22;
Pred. No. 4.1e-135;
2; Mismatches 11;
  Zhou
F, C
   2111
from
  u P,
Chen
   (AAK52582) and 3666 the sequence listing
                      Length 358;
  Xu C, Ca
  Cao Y
ang ZW;
 6
  ۲
   356
 Gaps
  therapy;
  Ma
  ĸ
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RESULT AND RESULT AND RESULT AND RESULT AND RESULT 
   뮍
  80
   В
  δÃ
   Вþ
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   Дb
   QΥ
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   QΥ
13-JUN-1997
13-JUN-1997
13-JUN-1997
13-JUN-1997
13-JUN-1997
13-JUN-1997
13-JUN-1997
13-JUN-1997
13-JUN-1997
13-JUN-1997
13-JUN-1997
13-JUN-1997
13-JUN-1997
13-JUN-1997
12-SEP-1997
12-SEP-1997
12-SEP-1997
12-SEP-1997
  02-OCT-1997;
13-JUN-1997;
13-JUN-1997;
  Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour, neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteopprosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
   Fragment of human secreted
   13-APR-1999
  179
  179
  119
   299
   299
   59
   59
  8
  MLARAARGHWGPFAEG--LSTGFWPRSGRASSGLPRNTVVLFVPQQEAWVVERMGRFHRI
||||||||
mlaraargtgalllrgsllasgrapr--rassglprntvvlfvpqqeawvvermgrfhri
  DIHVPPRVKESMOMQVEAERRKRATVLESEGTRESAINVAEGKKQAQILASEAEKAEQIN
   dihvpprvkesmqmqveaerrkratvlesegtresainvaegkkqaqilaseaekaeqin
   qaageasavlakakakaeairilaaaltqhngdaaasltvaeqyvsafsklakdsntill
  standard;
   (first entry)
97US-0061060.
97US-0049548.
97US-0049549.
97US-0049606.
97US-0049606.
97US-0049608.
97US-0049608.
97US-0049610.
97US-0049610.
97US-0049611.
97US-0049611.
97US-0050566.
97US-0050566.
97US-0050566.
97US-00508665.
97US-0058666.
  98WO-US12125
   Protein;
   protein encoded
   γď
   gene
   <u>3</u>5
   298
  238
  238
  178
  58
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RESULT
AAU28053
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   밁
   S
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  SSSSSS
  В
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  Query Match
Best Local Sim
Matches 341;
                    17-JUN-2000;
14-JUL-2000;
19-SEP-2000;
20-OCT-2000;
  ischaemia-reperfusion injury; haematopolesis; cancer; neuropathy; transgenic animal; Alzheimer's disease; parkinson's disease; burn; amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia; ulcer; osteoporosis; bone degenerative disorder; periodontal diseas; gut protection; lung; liver fibrosis; immune deficiency; infection;
   inflammation.
Note: Records for SEQ ID NO 2110 (AAK52581), (AAM80020) are omitted as the relevant pages were missing at the time of publication.
  07-MAR-2000;
19-MAY-2000;
  05-MAR-2001;
  WO200166689-A2
  severe combined immunodeficiency; SCID; autoimmune disorder; allergy; multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;
   Human; secreted
   Novel human
  18-DEC-2001
   AAU28053;
   Sequence
(HYSE-)
  13-SEP-2001
   fertility; analgesic;
   261
  201
   179
  141
   321
   299
  239
   119
   81
   59
  23
   1 MLARAARGHWGPFAEG--LSTGFWPRSGRASSGLPRNTVVLEVPQQEAWVVERMGREHRI
  6
  psnpgdvtsmvaqamgvygaltkapvpgtpdslssgssrdvqgtdasldeeldrvkms
   PSNPGDVTSMVAQAMGVYGALTKAPVPGTPDSLSSGSSRDVQGTDASXDEELDRVKMS
   DIHVPPRVKESMQMQVEAERRKRATVLESEGTRESAINVAEGKKQAOILASEAEKAEQIN 238
   mlaraargtgalllrgsllasgrapr--rassglprntvvlfvpqqeawvvermgrfhri
  QAAGEASAVLAKAKAEAIRILAAALTQHNGDAAASLTVAEQYVSAFSKLAKDSNTILL
   dihvpprvkesmqmqveaerrkratvlesegtresainvaegkkqaqilaseaekaeqin
  Similarity
 HYSEQ
   standard;
  378
                    2000US-0519705.
2000US-0574454.
2000US-0596193.
2000US-0616847.
2000US-0665363.
2000US-0693267.
  secretory protein,
   Conservative
  2001WO-US04942
  (first
  protein; arthritis; Crohn's disease; sepsis; shock;
   Protein;
  93.2%;
   pain;
  antigen
   3007
   2
  Score 1646; DB 22;
Pred. No. 4.8e-136;
2; Mismatches 11;
  Seq
   ID No
   222.
  2111 (AAK52582) and 3666 from the sequence listing
  Length
   Indels
   sequence
  378;
  4
   disease;
  listing
  Gaps
  140
  320
  298
   178
  118
  80
   200
  58
  2;
```

```
CC ischaemia-reperfusion injury shock, sepsis, immune responses, and is convolved in increasing haematopolesis, stem cell survival, bone growth can remodeling. (I), (II) and modulators of (II) are useful for comphylaxis or treatment of one or more cancers. (II) is also useful for creating transgenic animals useful for studying the in vivo activities of the polypeptide as well as for studying modulators of the polypeptides. (I) induces the proliferation of neural cells and regeneration of nerve can brain tissue and is useful for the treatment of central and contributes in addition, (I) is involved in chemotactic or chemokinetic sclerosis. In addition, (I) is involved in chemotactic or chemokinetic cactivity, regulation of haematopolesis and is useful for treating myeloid or lymphoid cell disorders, platelet disorders such as thrombocytopenia and for regeneration of bone, cartilage, tendon, ligament and/or nerve tissue growth, and in tissue repair, healing of burns, incisions, culters, for treating osteoporosis, osteoarthritis, bone degenerative constants or reperfusion injury in various tissues, various immune deficiencies and conference combined immunodeficiency (SCID), bacterial or fungal infections, autoimune disorders e.g. multiple sclerosis, in addition, (I) affects biorhythms or circadian cycles of rhythms, catabolism, catabolism, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides analized contents of ther pain reducing effects.
                             analgesic effects or other pain reducing effects, immuneglobulin like activity and can act as an antigen in a vaccine composition to raise an immune response. AAU28020-AAU28395 represent novel human secreted protein amino acid sequences of the invention.
   Tang
Zhao
   Novel polypeptides and nucleic acids obtained from prepared from various human tissues, for diagnosis cancer, neurological, inflammatory, and autoimmune
   WPI; 2001-589934/66.
N-PSDB; AAS44953.
   Example
  and polynucleotides (II). (I) and (II) are useful for treating inflammatory conditions such as arthritis, nephritis, Crohn's disease
   YT,
   ω
••
   Liu C,
Yang Y,
  SEQ ID No 222; 107pp; English
  relates to novel isolated human secreted polypeptides (I)
   Asundi V,
Drmanac
   RT,
  ×
   C, Wehrman
Zhang J, C
   Chen
  Ή.
  Ren
   cDNA libraries and treatment of disorders -
   л ғ,
хие
   Ма
AJ,
   Y, Zhou P;
Wang J;
   protein
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   밁
   Š
   밁
   Š
   В
   δ
  В
  Matches
  Query Match
Best Local Similarity
    239
                     239
   179
   179
   119
  119
  59
  59
  بر
  \mathbf{L}
LEPGLNILIPVLDRIRYVQSLKEIVINVPEQSAVTLDNVTLQIDGVLYLRIMDPYKASYG
  MLARAARGHWGPFAEG--LSTGFWPRSGRASSGLPRNTVVLEVPQQEAWVVERMGREHRI
   DIHVPPRVKESMQMQVEAERRKRATVLESEGTRESAINVAEGKKQAQILASEAEKAEQIN
  mlaraargtgalllrgsllasgrapr--rassglprntvvlfvpqqeawvvermgrfhri 58
                                       dihvpprvkesmqmqveaerrkratvlesegtresainvaegkkqaqilaseaekaeqin
   lepglnilipvldriryvqslkeivinvpeqsavtldnvtlqidgvlylrimdpykasyg
   Conservative
  93.0%;
  ω
••
  Score 1643;
Pred. No. 1
  Mismatches
  DB 22;
.5e-134;
   Length 3007;
   Indels
  4.
  Gaps
  178
  118
   58
                     298
  238
   118
  238
  'n
```

Sequence

3007

AA;

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cc or polypeptides in a sample, and methods of idetecting the nucleotides correctly peptides of the invention Although novel, many of the copypeptides of the invention have homology to known proteins, thereby cc giving an insight into their probable biological activities, and hence cc gotential therapeutic applications. The polypeptides of the invention may characterize activities; including cytokine, cell proliferation or cell cdifferentiation activities; stem cell growth factor activities; cc haematopoiesis regulatory activity; tissue growth activity; characterize conditions, cell proliferation or cell characterize conditions, cell proliferation or cell conditions, cell oncogenesis, cancer cell provides and nucleotides of the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell cancers), chronic inflammatory conditions (e.g., asthma or arthritis), corporary heart disease, carcers, haematopoietic disorders (e.g., osteoporosis), and abnormal cancersal ischaemia, bone disorders (e.g., osteoporosis), and abnormal cancertal ischaemia, bone disorders (e.g., osteoporosis), and abnormal cancertal ischaemia, bone disorders (e.g., osteoporosis), and abnormal cancertal ischaemia, some hambor of them may be used to promote wound healing (e.g., of burns, incisions and ulcers), while those with communications and communications and communications and communications and communications and communications and communications and communications and communications and communications and com
         밁
   Ş
  В
   Ş
  Query Match
Best Local S
Matches 341
  Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA0825-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides and the polypeptides, methods of detecting the nucleotides.
  Tang
  03-FEB-2000;
27-APR-2000;
   Claim 20; Page 291; 1963pp; English.
  e.g. arthritis
   Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject
   (HYSE-)
   05-FEB-2001;
   Sequence
   Local Similarity
         18
   59
  23
   -
   2001-457740/49
MLARAARGHWGPFAEG--LSTGFWPRSGRASSGLPRNTVVLFVPQQEAWVVERMGRFHRI 58
  mlaraargtgalllrgsllasgrapr--rassglprntvvlfvpqqeawvvermgrfhri
   341;
   HYSEQ INC
  Liu C,
  techniques. The present sequence represents a novel human
   378
   Conservative
  2000US-0496914.
2000US-0560875.
   2001WO-US03800
  and
  Drmanac
   cancer
  invention.
   93.2%;
   <u>ب</u>
   Score 1646; DB 22;
Pred. No. 4.8e-136;
   Mismatches
   Length
   Indels
   4:
   Gaps
   80
   2
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٠, د٠

leukaemia,

nervous

disorders,

arthritis and

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RESULT
AAM79550
δÃ
  B
  δÃ
   Вþ
  Qy
  Ър
   δÃ
  밁
  03-FEB-2000;
27-APR-2000;
20-JUN-2000;
19-JUL-2000;
  Human; cytokine; cell proliferation; cell differentiation; gene vaccine; peptide therapy; stem cell growth factor; haematopolesi tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
  06-NOV-2001 (first entry)
         activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or
                                 The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating
   Zhao
   01-SEP-2000;
   05-FEB-2001; 2001WO-US04098
  WO200157190-A2
  Homo sapiens
   Human protein
  AAM79550 standard; Protein; 378 AA.
   Claim
   Nucleic acids encoding polypeptides with cytokine-like activities
  15-SEP-2000;
20-OCT-2000;
   Xue AJ,
  (HYSE-)
  141
   299
   261
  S
   PSNPGDVTSMVAQAMGVYGALTKAPVPGTPDSLSSGSSRDVQGTDASXDEELDRVKMS
   dihvpprvkesmqmqveaerrkratvlesegtresainvaegkkqaqilaseaekaeqin
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  2001-476283/51.
DB; AAK52683.
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   20; Page 281-282; 6221pp; English.
   'n
  HYSEQ INC
   Wang L.
   diagnosis and
  Liu C,
   2000US-0560875.
2000US-0598075.
2000US-0620325.
2000US-0654936.
   2000US-0663561
2000US-0693325
   2000US-0496914
   2000US-0728422
  SEQ ID NO 3196
   , Wang J,
Wejhrman
  Drmanac F
Wang J,
  gene
  c RT, Asundi V,
J, Zhang J, Ren |
an T, Goodrich R;
  therapy
   æ
   Zhou
  Chen
  Ŗŭ
   haematopoiesis;
   Wang
   Cao 1
   378
  therapy;
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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dr primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises an eoilgonucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 5'-end sequence complementary to a polynucleotide which comprises a 5'-end sequence complementary to a
   Claim 8;
  and/or
  29-JUL-1999; 99JP-0248036.
27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899.
   Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
   full-length cDNAs
   07-FEB-2001
  EP1074617-A2
  Human; primer;
  Human protein
   (HELT-) HELIX RES INST
   28-JUL-2000; 2000EP-0116126
   26-JUN-2001
   AAB92659
  119
  299
   299
  179
   179
   59
  59
   w
   PSNPGDVTSMVAQAMGVYGALTKAPVPGTPDSLSSGSSRDVQGTDASXDEELDRVKMS
   2001-318749/34.
   psnpgdvtsmvaqamgvygaltkapvpgtpdslssgssrdvqgtdasldeeldrvkms
  VEDPEYAVTQLAQTTMRSELGKLSXDKVFRERESLNASIVDAINQAADCWGIRCLRYEIK
   LEPGLNILIPVLDRIRYVOSLKEIVINVPEQSAVTLDNVTLQIDGVLYLRIMDPYKASYG
   mlaraargtgalllrgsllasgrapr--rassglprntvvlfvpqqeawvvermgrfhri
  lepglnilipvldriryvqslkeivinvpeqsavtldnvtlqidgvlylrimdpykasyg
   Ś
   Isogai T,
3, Sugiyama
   SEQ ID 11010;
   standard;
  (first
  sequence SEQ ID NO:11010
  detection; diagnosis; antisense therapy; gene therapy
   Nishikawa
m T, Wakama
   Protein;
  entry)
  2537pp +
  nikawa T, Ha
Wakamatsu A,
   356
  G
   Hayashi K,
A, Nagai K,
  ROM;
  English
  Saito K,
   Otsuki
   +
  Yamamoto
  Ų,
  298
  178
   58
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δÃ
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   3333333333333XX
       뮍
   δÃ
  Query
Best L
   Matches
   the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length CDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention.
  Sequence
  oligonucleotide comprises at least 15 nucleotides and the combinati
   179
   179
  119
       299
                                 299
   239
  119
  59
  59
  Local Similarity
  l mlaraargtgalllrgsllasgrapr--rassglprntvvlfvpqqeawvvermgrfhri
  1 MLARAARGHWGPFAEG--LSTGFWPRSGRASSGLPRNTVVLFVPQQEAWVVERMGRFHRI
   Match
   PSNPGDVTSMVAQAMGVYGALTKAPVPGTPDSLSSGSSRDVQGTDASXDEELDRVKMS 356
  VEDPEYAVTQLAQTTMRSELGKLSXDKVFRERESLNASIVDAINQAADCWGIRCLRYEIK 178
   QAAGEASAVLAKAKAKAEAIRILAAALTQHNGDAAASLTVAEQYVSAFSKLAKDSNTILL
  341;
  356
   Conservative
  AΑ;
   93.2%;
95.3%;
  2;
   Score 1646; DB 22;
Pred. No. 4.4e-136;
   Mismatches
   nucleotides and the combination of
  Indels
  Length
  4
  Gaps
   178
  58
  ij
  N
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ABB11981
ID ABB11981 standard; peptide; 378 AA.
XX
AC ABB11981;
XX
DT 11-JAN-2002 (first entry)
XX
XX
DE Human SLP-2 homologue, SEQ ID NO:2351.
XX
XX
Human; cytokine; cell proliferation; c
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Human; cytokine; cell proliferation; cell differentiation; growth factor; haematopoiesis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemotaresis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiinflammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic; cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial; antiinfngal; vulnerary; antiulcer.

Homo sapiens

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RESULT
AAW78160
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   밁
   δÃ
   Вb
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  В
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  Query Match
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Matches 356
   The present sequence represents human integral membrane protein (IMP). IMP may be administered to a subject to treat disorders associated with abnormal ion transport or membrane conductance as well as a variety of tumours, e.g. haemolytic anaemias and prostate, breast and pancreatic tumours. A vector capable of expressing IMP, or a fragment or a derivative thereof, may also be administered to a subject to treat the haemolytic anaemias and prostate, breast and pancreatic tumours.
  Goli
   Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
  Sequence
   Claim 1;
   DNA encoding human integral membrane protein - recombinant protein, for treatment of anaemia \epsilon
  N-PSDB;
WO9856804-A1
  Human secreted
  AAW78160 standard;
                         Homo sapiens
   endocrine;
   AAW78160
   301
   301
  241
   181
  181
   121
  121
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   61
   N
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  1998-347418/30
  SK,
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  AGEASAYLAKAKAKAEAIRILAAALTQHNGDAAASLTVAEQYVSAFSKLAKDSNTILLPS
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   Similarity
  AAV28867
   Column
  Hillman JL;
  356 AA;
  metabolism;
  99.8%; Score 1763; DB 19; ilarity 100.0%; Pred. No. 2.4e-146; Conservative 0; Mismatches 0;
   (first
  protein encoded by
   35-38;
  Protein;
   entry)
  33pp; English
   regulation;
  ⋧
  gene 35 clone HTXCS21.
  anaemia and
   useful for
  Length 356;
  cancer
   Indels
   gastritis; neoplasm
  producing
   0;
   Gaps
  300
   180
   60
  60
  300
   240
   0;
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1 MLARAARGHWGPFAEG--LSTGFWPRSGRASSGLPRNTVVLFVPQQEAWVVERMGRFHRI

Query Match Best Local Similarity

93.2%;

Score 1646; DI Pred. No. 4.4e 2; Mismatches

DB 20; 1.4e-136; nes 11;

Indels Length

Gaps

2

58

356; 4.

Matches

Conservative

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13-JUN 1997
08-JUL 1997
18-AUG-1997
12-SEP 1997
02-OCT 1997
02-OCT 1997
02-OCT 1997
   13-JUN-1997;
13-JUN-1997;
13-JUN-1997;
13-JUN-1997;
                            This sequence represents a secreted human protein encoded by the gene clone detailed in the descriptor line. The gene can be used to generat fusion proteins by linking to the gene to a human immunoglobulin Fc portion (e.g. AAXV4302) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to 86 novel genes and their fragments (nucleic acid sequences: AAXV4301-XV4410; amino acid sequences AAXV8126-W78225) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polynucleotides. Specific uses are described for each of the 86 polynucleotides, based on which tissues they are most highly expressed
  Brewer
Moore F
  New isolated human genes and the secreted polypeptides they encode useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
   Claim 11; Page 282-283; 380pp; English.
   N-PSDB; AAX04345
   WPI; 1999-080881/07
   Yu GL;
   13-JUN-1997;
13-JUN-1997;
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   13-JUN-1997
   13-JUN-1997
  13-JUN-1997
13-JUN-1997
  (HUMA-) HUMAN
   13-JUN-1997
Sequence
                      AAX04311 for described uses).
  PA,
  N.
356
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Ni J,
   GENOME SCI INC
   97US-0055984.

97US-0058668.

97US-0058668.

97US-005869.

97US-0058975.

97US-0058972.

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  97US-0049549
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  97US-0061060
  98WO-US12125
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  ,SH
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Rosen
  n CA,
  y P,
Ruben
  Greene JM,
ben SM, Shi
  Lafleur DW;
Y, Young P
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to generate
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Title:
Perfect score:
Sequence:
  Result
No.
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   Database
  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
   Total number of hits satisfying chosen parameters:
  Searched:
  Scoring table:
   OM protein - protein search, using sw model
  9
  110
110
110
   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 1646
1646
1646
1646
1643
1643
1635
1493
1493
1064.5
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  Match Length DB
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  US-09-898-216-1
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1 MLARAARGHWGPFA
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A_Geneseq_032802:*

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   747574 seqs, 111073796 residues
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    356
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323
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AAU331588
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643.173 Million cell update
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  747574
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Human SLP-2 homolo
Human protein SEQ
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AAW57232
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## ALIGNMENTS

Human; integral membrane protein; IMP; cancer; anaemia; prostate; breast; pancreatic; tumour; ion transport. 03-AUG-1998 (first entry) Human integral membrane protein. AAW57232;

AAW57232 standard; Protein;

356

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   09-JUN-1998.
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                       97US-0781562
   97US-0781562
   /note= "encoded by 346
  /label= unknown
/note= "encoded
  bу
   by NTG
   NTT.
   CTN"
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  밁
  Query Match
Best Local Similarity
Matches 26; Conserv
   This sequence represents a fragment of a secreted human protein encoded by the nucleic acid molecule detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Fc portion (e.g. AAX04302) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to 86 novel genes and their fragments (nucleic acid sequences: AAX04311-X04410; amino acid sequences AAX078126-W78225) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 86 polynucleotides, based on which tissues they are most highly expressed in a sample or which tissues they are most highly expressed in the form of the second which tissues they are most highly expressed in the form of the form of the second
  13-JUN-1997
13-JUN-1997
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13-JUN-1997
108-JUL-1997
12-SEP-1997
12-CCT-1997
02-CCT-1997
02-CCT-1997
   13-JUN-1997;
13-JUN-1997;
13-JUN-1997;
13-JUN-1997;
13-JUN-1997;
   New isolated human genes and the secreted polypeptides they encode useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
  WPI; 1999-080881/07.
N-PSDB; AAX04345.
  Brewer LA, Ebner R, Ferrie AM, Moore PA, Ni J, Olsen HS, Ros
  Sequence
  Disclosure; Page 35; 380pp; English.
   ĭ
   (see
  11-JUN-1998;
   (HUMA-) HUMAN GENOME SCI INC.
  13-JUN-1997;
13-JUN-1997;
                   276 LTVAEQYVSAFSKLAKDSNTILLPSN 301
1 ltvaeqyvsafsklakdsntillpsn 26
   AAX04311 for described uses).
  26
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970S-0050566

970S-0050566

970S-005091

970S-005091

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  98WO-US12125
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KW AINFI
  Ş
  В
  Query Match
Best Local S
Matches 27
13-JUN-1997
13-JUN-1997
08-JUN-1997
18-AUG-1997
12-SEP-1997
12-SEP-1997
12-SEP-1997
12-SEP-1997
12-SEP-1997
12-SEP-1997
12-SEP-1997
  13-JUN-1997;
13-JUN-1997;
13-JUN-1997;
  Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
   stability of the fused protein as compared to the human protein only. The invention relates to 86 novel genes and their fragments (nucleic acid sequences: AAX04311-X04410; amino acid sequences AAX04311-X04410; which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polymerides in a sample or by determining the presence of mutations in the new polymecleotides. Specific uses are described for each of the 86 polymereotides, based on which tissues they are most highly expressed in (see AAX04311 for described uses).
  02-OCT-1997;
13-JUN-1997;
   human immunoglobulin Fc portion (e.g. AAX04302) for increasing stability of the fused protein as compared to the human protein
  13-JUN-1997;
13-JUN-1997;
  13-JUN-1997;
13-JUN-1997;
   13-JUN-1997;
   13-JUN-1997;
  11-JUN-1998;
   17-DEC-1998
  WO9856804-A1
  Fragment of human secreted protein encoded by
  AAW78285 standard; Protein; 26
   Sequence
   13-JUN-1997;
   190 MOMOVEAERRKRATVLESEGTRESAIN 216
  14
   1 mqmqveaerrkratvlesegtresain 27
  l Similarity
27; Conserv
   27 AA;
  Conservative
  (first entry)
97US-0055984.
97US-0058665.
97US-0058668.
97US-0058669.
97US-0058750.
97US-0058971.
97US-0058972.
   97US-0049611.
97US-0050566.
97US-0050901.
97US-0052989.
97US-0051919.
  97US-0049550.
97US-0049606.
97US-0049607.
97US-0049608.
  97US-0049609
   97US-0049548
97US-0049549
  98WO-US12125
  7.6%; out
100.0%; Pr
  Score 27; DB; Pred. No. 6.9
0; Mismatches
  DB 20; 1
6.9e-19;
   gene
   Length 27;
  0;
   Gaps
  0
```

```
QΥ
  밁
   Query Match
Best Local S
Matches 26
   12-SEP-1997;
02-OCT-1997;
02-OCT-1997;
02-OCT-1997;
02-OCT-1997;
02-OCT-1997;
02-OCT-1997;
   This sequence represents a fragment of a secreted human protein encoded by the nucleic acid molecule detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Fc portion (e.g. AAXV4302) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to 86 novel genes and their fragments (nucleic acid sequences: AAXV4311-XV4410; amino acid sequences AAWV8126-W78225) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polynucleotides. Specific uses are described for each of the 86 polynucleotides, based on which tissues they are most highly expressed in see aaxV4311 for described uses in the new polynucleotides. Specific uses are described for each of the 86 polynucleotides, based on which tissues they are most highly expressed in the new polynucleotides.
  Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
   AAW78287
   New isolated human genes and the secreted polypeptides they encode useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
  cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
   13-APR-1999
   Sequence
  Disclosure;
   WPI; 1999-080881/07
N-PSDB; AAX04345.
  Brewer
  Fragment of
   Moore PA,
  ( HUMA - )
  115 ASYGVEDPEYAVTQLAQTTMRSELGK 140
   1 asygvedpeyavtqlaqttmrselgk 26
  GL;
   l Similarity 100 26; Conservative
  HUMAN GENOME
   standard;
  human secreted protein encoded by
  Page
   Ebner R, Fe
Vi J, Olsen
   (first entry)
   AA;
   for described uses).
   97US-0058975.
97US-0060834.
97US-0060841.
97US-0060844.
97US-0060865.
97US-0061059.
  35;
   Protein;
   7.3%;
  SCI
  380pp; English.
  Ferrie
  regulation; malabsorption;
   HS,
   0;
   26
  Score 26;
Pred. No.
  AM,
   Rosen
   A
   Mismatches
   Feng P, Greene
n CA, Ruben SM,
  DB 20;
, 6.3e-18;
0;
   Greene JM, Laf
ben SM, Shi Y,
  gene
  Length 26;
  gastritis; neoplasm.
   Indels
  Lafleur DW; Y, Young P;
   0;
   0
```

```
밁
                                     á
   CC ischaemia reperfusion injury, shock, sepsis, immune responses, and is can velocity the involved in increasing haematopolesis, stem cell survival, bone growth can remodeling. (I), (II) and modulators of (II) are useful for growth can remodeling. (I), (II) and modulators of (II) are useful for coreating transgence animals useful for studying the in vivo activities of the polypeptide as well as for studying modulators of the polypeptides. (I) induces the proliferation of neural cells and regeneration of nerve cancers (II) is also useful for the polypeptides. (I) induces the proliferation of neural cells and regeneration of nerve can disease, and an animal suseful for the treatment of central and continuity, regulation of haematopoiesis and is useful for treating myeloid call disorders, platelet disorders such as Alzheimer's, cativity, regulation of haematopoiesis and is useful for treating myeloid call disorders, platelet disorders such as thrombocytopenia and for regeneration of bone, cartilage, tendon, ligament and/or nerve culcers, for treating osteoporosis, osteoarthritis, bone degenerative construction or regeneration and treatment of lung or liver fibrosis, captilage, tendon, ilgament and/or nerve culcers, for treating osteoporosis, osteoarthritis, bone degenerative construction of periodontal disease. Purthemore, (I) is also useful for the periodontal disease, various immune deficiencies and constitution, and treatment of lung or liver fibrosis, captilage, treatment of lung or liver fibrosis, constitution of the periodontal disease, various immune deficiencies and constitutions, such as asthma or other respiratory problems. (I) affects biorhythms or circadian cycles of rhythms, carabolism, anabolism, storage or elimination of constity and can act as an antigen in a vaccine composition to raise an immune response. ANU28020-ANU28395 represent novel human secreted protein amino acid sequences of the invention.
   Query Match
Best Local
   17-JUN-2000;
14-JUL-2000;
19-SEP-2000;
  Tang
Zhao
  Sequence
   Example 2; SEQ ID No 598; 107pp; English.
   Novel polypeptides and nucleic acids obtained from cDNA libraries prepared from various human tissues, for diagnosis and treatment of cancer, neurological, inflammatory, and autoimmune disorders -
   (HYSE-)
   07-MAR-2000;
  05-MAR-2001;
  13-SEP-2001.
  and polynucleotides (II). (I) and (II) are useful for treating inflammatory conditions such as arthritis, nephritis, Crohn's disease,
  19-MAY-2000;
     108
   27
  invention relates to novel isolated human secreted polypeptides
                RASSGLPRNTVVLEVPQQEAWVVERMGRFHRILEPGLNILIPVLDRIRYV 76
rassglprntvvlfvpqqeawvvermgrfhrilepglnilipvldriryv 157
  QA,
  2001-589934/66.
DB; AAS45141.
  50;
   Similarity
   HYSEQ INC
   Liu (
  463
   2000US-0519705.
2000US-0594454.
2000US-0596193.
2000US-0616847.
2000US-0665363.
2000US-0693267.
  Conservative
   , X, 1, C,
  2001WO-US04942
  AA;
   Asundi V,
   14.0%; 500
100.0%; Pr
  Drmanac RT,
   Score; Pred.
   Xu C, Wehrma
T, Zhang J,
  Mismatches
   . 50;
   Wehrman T, Ke
ing J, Chen R,
   DB 22; I
2.7e-40;
  Length 463;
   Ren
  Xue
   Ē
  Ą
   Ma
   Wang
   0
   Zhou
  Gaps
   Ρ,
   0
```

RESULT

This sequence represents a fragment of a secreted human protein ence by the nucleic acid molecule detailed in the descriptor line. The can be used to generate fusion proteins by linking to the gene to a

n encoded The gene

Disclosure; Page 35; 380pp; English.

New isolated human genes and the secreted polypeptides they encode useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders

Brewer LA, Moore PA,

N. Ebner

ŭ,

Olsen

Ferrie HS,

Rosen Α Μ,

Feng n CA,

y P, Ruben

Greene JM, ben SM, Shi

Lafleur DW; Y, Young P

φ,

1999-080881/07. DB; AAX04345.

```
AAW78286
ID AAW7
13-JUN 1997;
08-JUL 1997;
18-AUG 1997;
12-SEP-1997;
   13-JUN-1997;
13-JUN-1997;
13-JUN-1997;
  Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
   cognitive disorder; schizophrenia; prostate; obesity; osteoc. osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; endocrine; metabolism; regulation; malabsorption; gastritis;
   AAW78286 standard; Protein;
   (HUMA-)
   02-OCT-1997
  02-OCT-1997
   13-JUN-1997
  13-JUN-1997
13-JUN-1997
  02-OCT-1997
   11-JUN-1998;
   WO9856804-A1
   Homo sapiens
  Fragment of human secreted protein encoded by
  13-APR-1999
   AAW78286;
  13-JUN-1997
  13-JUN-1997
  13-JUN-1997
   13-JUN-1997
  13-JUN-1997
   13-JUN-1997
   HUMAN
  (first entry)
   GENOME
   97US-0060841.
97US-0060844.
97US-0060865.
97US-0061059.
   97US-
97US-
  97US-
  97US-0058971
97US-0058972
   97US-0058669
97US-0058750
   97US-0058665
97US-0058668
   97US-0050566
97US-0050901
  97US-0049610
97US-0049611
   97US-0049608
97US-0049609
  97US-0049547
97US-0049548
  97US-0060834
   97US
  97US
   97US-0049607
   97US-0049606
   97US-0049550
   97us-0061060
   98WO-US12125
   -0058975
  -0049549
   SCI INC
  27
   AA
   gene
   osteoclast; thymus;
  digestion; neoplasm.
```

```
RESULT 1
QΥ
   Вb
  δÃ
  В
  polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide and cells genetically the nucleic acids encoding the polypeptide vectors comprising the nucleic acids encoding the polypeptide vectors comprising the proteins are useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoissis; and in Co bone, cartilage, tendon and/or nerve tissue growth or regeneration; continue suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. ANU29510-AAU33304 represent the amino acid sequences of novel human secreted proteins of the invention.
   Query Match
  Matches
   Claim 20; Page 716; 765pp; English.
  Tang
Homo sapiens.
                                nervous
  Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia;
   Human polypeptide
  06-NOV-2001
   AAO09538 standard; Protein; 92 AA
  Sequence
   The invention relates
  vaccination, testing and therapy
   Nucleic acids encoding a
   (HYSE-) HYSEQ INC.
  18-APR-2000; 2000US-0552929; 26-JAN-2001; 2001US-0770160;
  16-APR-2001; 2001WO-US08656
   WO200179449-A2
   Homo sapiens
   87
  87
   27
   27
   Local
   RASSGLPRNTVVLFVPQQEAWVVERMGRFHRILEPGLNILIPVLDRIRYVQSLKEIVINV 86
   PEQSAVTLDNVTLQIDGVLYLRIMDPYKASYGVEDPEYAVTQLAQTTMRSELGKLS 142
  peqsavtldnvtlqidgvlylrimdpykasygvedpeyavtqlaqttmrselgkls 142
   rassglprntvvlfvpqqeawvvermgrfhrilepglnilipvldriryvqslkeivinv 86
  116;
  Similarity
                              system
  Liu C,
  222
  32.6%; ilarity 100.0%; Conservative
  (first entry)
  Ą,
                                disorders; arthritis;
  Drmanac RT
   SEQ ID
   to novel
   NO 23430
   range of human polypeptides, useful in
  0;
  Score 116; DB 22;
Pred. No. 3.2e-105;
   human secreted
  Mismatches
                                inflammation.
   polypeptides.
  0,
   Length 222;
  Indels
  0;
  Gaps
   genetic
  0
```

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RESULT 12
AAU28241
  рЬ
  Š
   Matches
   Query Match
Best Local
   the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynectices and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating activity tissue growth factor activity, immunomodulatory activity and activinyinhibin activity and may be useful in the diagnosis and/or regiment of cancer lawlesses.
  Human; secreted protein; arthritis; Crohn's disease; sepsis; shock; ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy; transgenic animal; Alzheimer's disease; Parkinson's disease; burn; amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia; ulcer; osteoporosis; bone degenerative disorder; periodontal disease; gut protection; lung; liver fibrosis; immune deficiency; infection; severe combined immunodeficiency; SCID; autoimmune disorder; allergy; multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;
   Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
  The
  Claim 20; SEQ ID NO 23430; 1399pp + Sequence Listing; English.
   Tang YT,
   Novel human secretory protein, Seq ID No 598.
  AAU28241 standard; Protein; 463
   Sequence
  treatment of cancer, leukaemia,
   Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immun
  28-FEB-2000; 2000US-0515126
18-MAY-2000; 2000US-0577409
  26-FEB-2001; 2001WO-US04927
   WO200164835-A2.
                              Homo sapiens
  18-DEC-2001
  inflammation
  fertility; analgesic;
   294 NTILLPSNPGDVTSMVAQAMGVYGALTKAPVPGTPDSLSSGSSRDVQGTDAS 345
  30 ntillpsnpgdvtsmvaqamgvygaltkapvpgtpdslssgssrdvqgtdas 81
  invention relates to human polynucleotides (AAI79941-AAI93841) and
   2001-514838/56
   Similarity
  HYSEQ
   Liu C,
   92 AA;
   Conservative
   (first entry)
  INC
  Drmanac RT
   14.6%;
  pain; antigen
   0,
   Score 52;
Pred. No.
  Ą
   Mismatches
  nervous system disorders, arthritis and
   DB 22; I
   0;
   Length 92,
   Indels
   immune
   0;
   Gaps
  6
   0
```

```
RESULT
AAU31S
ID AAU3
XX AAU3
XC AAU3
XX B-D
DT 18-D
XX Nove
XX Nove
XX Stem
KW Stem
KW Inmu
   g
   Ş
  В
  5
  В
   Ş
  밁
  Š
   В
   Ş
   Query Match
Best Local :
  encoded polypeptides (AAM/8323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, inmunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
  Tang YT,
Zhao QA,
Xue AJ,
            Human; vaccination; gene therapy; nutritional supplement; stem cell proliferation; haematopoiesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemi
  Novel human secreted protein
  AAU33159 standard; Protein; 2797 AA
   Sequence
   Inflammation.

Note: Records for SEQ ID NO 2110 (AAK52581), 2111
(AAM80020) are omitted as the relevant pages from were missing at the time of publication.
  The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
  Claim 20; Page 3486-3487; 6221pp; English.
  Nucleic acids encoding useful in diagnosis and
   30-NOV-2000; 2000US-0728422
   18-DEC-2001
  (HYSE-)
  207
  207
  147
  147
   87
   87
   27
   27
   Local
   9
   SEGTRESAINVAEGKKQAQILASEAEKAEQINQAAGEASAVLAKAKAKAEAIRILAAALT 266
   FRERESLNASIVDAINQAADCWGIRCLRYEIKDIHVPPRVKESMOMQVEAERRKRATVLE 206
  RASSGLPRNTVVLFVPQQEAWVVERMGREHRILEPGLNILIPVLDRIRYVQSLKEIVINV 86
  segtresainvaegkkqaqilaseaekaeqinqaageasavlakakakaeairilaaalt 266
  PEQSAVTLDNVTLQIDGVLYLRIMDPYKASYGVEDPEYAVTQLAQTTMRSELGKLSXDKV 146
   frereslnasivdainqaadcwgirclryeikdihvpprvkesmqmqveaerrkratvle 206
  Similarity
   Liu C, Drmanac RT,
Wang D, Wang J, Z
Yang Y, Wejhrman T,
   358 AA;
   Conservative
  (first entry)
  Drmanac RT, Asundi V, Zhou
, Wang J, Zhang J, Ren F, (
Wejhrman T, Goodrich R;
   and
  55.6%;
99.7%;
  polypeptides with cytokine-like activities
d gene therapy -
   0;
  Score 198; DB 22; Length 358; Pred. No. 2.5e-185;
   Mismatches
  Chen
  Ψ,
   (AAK52582) and 3666 the sequence listing
   Indels
  Xu C, Ca
  Cao Y,
               leukaemia
   0
  Gaps
  Ma
  Υ,;
   0
```

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Q
  RESULT 10
AAU33158
   δÃ
  Вþ
  DЬ
  The invention relates to novel human secreted polypeptides. The CC polypeptides and antibodies to the polypeptides are useful for CC determining the presence of or predisposition to a disease associated CC with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or CP physiological interactions of the polypeptide. Vectors comprising CC the nucleic acids encoding the polypeptides and cells genetically cengineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and CC therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in CC bone, cartilage, tendon and/or nerve tissue growth or regeneration; CC immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid CC sequences of novel human secreted proteins of the invention.
  Query Match
Best Local Similarity
Matches 123; Conserv
  AAU33158 standard; Protein;
   Sequence
  Claim 20; Page 716; 765pp; English.
  Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy - \,
   Novel human secreted protein #3649
  WPI; 2001-611725/70
  Tang
   (HYSE-) HYSEQ INC.
   18-APR-2000;
26-JAN-2001;
  16-APR-2001; 2001WO-US08656
   Homo sapiens.
   121
   343 DAS
  283 VSAFSKLAKDSNTILLPSNPGDVTSMVAQAMGVYGALTKAPVPGTPDSLSSGSSRDVQGT 342
   223
  61
   das
  vsafsklakdsntillpsnpgdvtsmvaqamgvygaltkapvpgtpdslssgssrdvqgt 120
  YT,
  123
  Liu C, Drmanac
   2797
  34.6%; Score 123; DB 22; 1 ilarity 100.0%; Pred. No. 4.5e-111; Conservative 0; Mismatches 0;
  2000US-0552929
2001US-0770160
   (first entry)
   AA;
  RT
  Length 2797;
  0
  Gaps
  6
```

0;

Human; vaccination; gene therapy; nutritional supplement; stem cell proliferation; haematopoiesis; nerve tissue regeneration;

anti-inflammatory;

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327

345

'n

```
В
  78284
  08-JUL-1997
18-RUG-1997
12-SEP-1997
12-SEP-1997
12-SEP-1997
12-SEP-1997
12-SEP-1997
12-SEP-1997
12-SEP-1997
12-SEP-1997
02-OCT-1997
02-OCT-1997
02-OCT-1997
   13-JUN-1997;
13-JUN-1997;
13-JUN-1997;
   13-JUN-1997;
13-JUN-1997;
  Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenceis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
  New isolated human genes useful for diagnosis and
  ľ
  Moore PA,
   13-JUN-1997;
13-JUN-1997;
  02-OCT-1997;
13-JUN-1997;
   11-JUN-1998;
   17-DEC-1998
   WO9856804-A1
   Homo sapiens
   endocrine;
  Fragment of human secreted
  13-APR-1999
  AAW78284;
   AAW78284 standard; Protein;
   (HUMA-)
   13-JUN-1997;
  13-JUN-1997;
  13-JUN-1997
13-JUN-1997
  13-JUN-1997;
   327
  7
   TPDSLSSGSSRDVQGTDAS
                                1999-080881/07.
DB; AAX04345.
  HUMAN
   metabolism; regulation; malabsorption; gastritis;
  Ebner
   (first entry)
  ŗ
  GENOME
   970S-0058669
970S-0058750
970S-0058971
970S-0058972
970S-0058875
970S-0050834
970S-0060834
  97US-0049611.
97US-0050566.
97US-0050901.
97US-0052989.
97US-0051919.
97US-00558665.
97US-0058668.
   97US-0049608.
97US-0049609.
97US-0049610.
   97US-0060844
97US-0060865
   98WO-US12125
   R, Fe
Olsen
  SCI INC
  Ferrie
   ,SH
and the secreted polypeptides they encode treatment of e.g. cancers, neurological % \left( 1\right) =\left( 1\right) ^{2}
   345
   protein encoded by
   306
  A,
   Rosen
   ₿
   Feng P, Greene JM,
n CA, Ruben SM, Shi
   gene
  35
   Lafleur DW;
Y, Young F
   neoplasm
  φ.
```

```
RESULT
AAM78566
  밁
  Qy
  В
  δÃ
  B
   ρ
   밁
  Qγ
   Query Match
Best Local S
Matches 202
03-FEB-2000;
27-APR-2000;
20-JUN-2000;
19-JUL-2000;
01-SEP-2000;
15-SEP-2000;
20-OCT-2000;
   by the nucleic acid molecule detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Fc portion (e.g. AAX04302) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to 86 novel genes and their fragments (nucleic acid sequences: AAX04311-X04410; amino acid sequences AAW78126-W78225) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 86 polynucleotides, based on which tissues they are most highly expressed is (see AAX04311 for described uses).
   Human; cytokine; cell proliferation; cell differentiation; gene the vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; rancon lands.
  disorders, immune diseases, inflammation or blood disorders
   05-FEB-2001;
   09-AUG-2001.
   Human protein
   06-NOV-2001
  AAM78566 standard; Protein; 358
   Sequence
   324
  144
  214
   154
   204
   94
   Local Similarity
les 202; Conserv
   8
   vpgtpdslssgssrdvqgtdas
  VPGTPDSLSSGSSRDVQGTDAS
  vlesegtresainvaegkkgaqilaseaekaeqingaageasavlakakakaeairilaa
  sequence represents a fragment of a secreted human
   306 AA;
   Page
            2000US-0496914
2000US-0560875
2000US-0598075
2000US-0620325
2000US-0654936
2000US-0663561
   Conservative
  2001WO-US04098
  (first entry)
   factor; immunomodulatory; cancer; ]
n disorder; arthritis; inflammation
  SEQ ID NO
  35; 380pp; English.
   56.7%; Score 202; DB 20; 100.0%; Pred. No. 2.6e-189; Live 0; Mismatches 0;
  1228
   345
  295
   Length 306;
  protein
   0;
   Gaps
  encoded
   273
  213
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   Matches
                                07-MAR-2000; 2000US-0519705.
19-MAY-2000; 2000US-0594193.
17-JUN-2000; 2000US-0596193.
14-JUL-2000; 2000US-0616847.
19-SEP-2000; 2000US-0665363.
   Homo
  ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy; transgenic animal; Alzheimer's disease; barkinson's disease; burn; amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia; ulcer; osteoporosis; bone degenerative disorder; periodontal disease gut protection; lung; liver fibrosis; immune deficiency; infection;
  inflammation.

Note: Records for SEQ ID NO 2110 (AAK52581), (AAM80020) are omitted as the relevant pages were missing at the time of publication.
  gut protection; lung; liver fibrosis; immune deficiency; information of immunodeficiency; SCID; autoimmune disorder; multiple sclerosis; rheumatoid arthritis; diabetes mellitus;
   05-MAR-2001;
   13-SEP-2001
   WO200166689-A2.
  rertility; analgesic;
   Novel human
  AAU28053;
   Sequence
  327
   349
  289
   267
  229
   207
   169
   147
   109
   Local (
  87
  49
  27
  6
   tpdslssgssrdvqgtdas
   TPDSLSSGSSRDVQGTDAS
  FRERESLNASIVDAINQAADCWGIRCLRYEIKDIHVPPRVKESMOMQVEAERRKRATVLE 206
   PEQSAVTLDNVTLQIDGVLYLRIMDPYKASYGVEDPEYAVTQLAQTTMRSELGKLSXDKV 146
  RASSGLPRNTVVLFVPQQEAWVVERMGRFHRILEPGLNILIPVLDRIRYVQSLKEIVINV
   segtresainvaegkkqaqilaseaekaeqinqaageasavlakakakaeairilaaalt
  SEGTRESAINVAEGKKQAQILASEAEKAEQINQAAGEASAVLAKAKAKAEAIRILAAALT 266
  peqsavtldnvtlqidgvlylrimdpykasygvedpeyavtqlaqttmrselgklsldkv
   rassglprntvvlfvpqqeawvvermgrfhrilepglnilipvldriryvqslkeivinv 108
   al Similarity
318; Conser
   secreted protein; arthritis; Crohn's disease; sepsis;
HYSEQ
  standard;
   378
   secretory protein,
   Conservative
   2001WO-US04942
   Protein;
   entry)
   61.2%;
99.7%;
  pain; antigen
   345
   0
   Score 218; DB 22;
Pred. No. 6.9e-205;
  Seq
  Mismatches
   IJ
  No 222
  2111
from
   Length 378;
   (AAK52582) and 3666
the sequence listing
  Indels
  0
  allergy;
   disease;
   shock;
  Gaps
  168
   348
  0
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the polypeptide as well as for studying modulators of the polypeptides.

(I) induces the proliferation of neural cells and regeneration of nerve and brain tissue and is useful for the treatment of central and peripheral nervous system diseases and neuropathies, such as Alzheimer's, comparison's disease, Huntington's disease, and amyotrophic lateral comparisons. In addition, (I) is involved in chemotactic or chemokinetic comparisons are consistent of the contract of comparisons are consistent of the contract of the contra
  and remodeling. (1), (II) and modulators of the invivo activities of prophylaxis or treatment of one or more cancers. (II) is also useful for creating transgenic animals useful for studying the in vivo activities of the polypeptide as well as for studying modulators of the polypeptides.

(I) induces the proliferation of neural cells and regeneration of nerve
   Tang
Zhao
  Novel polypeptides and nucleic acids obtained from cDNA libraries prepared from various human tissues, for diagnosis and treatment cancer, neurological, inflammatory, and autoimmune disorders -
  ischaemia-reperfusion injury, shock, sepsis, immune responses, and involved in increasing haematopoiesis, stem cell survival, bone ground remodeling. (I), (II) and modulators of (II) are useful for the contraction
  Example 3;
   N-PSDB;
  inflammatory conditions such as arthritis, nephritis, Crohn's disease
  polynucleotides (II). (I) and (II) are useful for treating
   invention relates to novel isolated human secreted polypeptides
   2001-589934/66
DB; AAS44953.
   YT,
  Liu (
   SEQ ID No
   Asundi V,
Drmanac
  222; 107pp; English.
   RT,
  Xu C, We
T, Zhang
   Wehrman T,
ng J, Chen
  'n
   ₩,
  Ren
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   Ма
АJ,
  a Y,
Wang
   bone growth
  Zhou
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Sequence Ã,

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disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, autoimmune disorders e.g. multiple sclerosis, rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic reactions and conditions, such as asthma or other respiratory problems. In addition, (I) affects biorhythms or circadian cycles of rhythms, fertility, metabolism, catabolism, anabolism, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides

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   Query Match
Best Local S
Matches 318
   147
  147
  87
  87
  27
  27
PEQSAVTLDNVTLQIDGVLYLRIMDPYKASYGVEDPEYAVTQLAQTTMRSELGKLSXDKV 146
  SEGTRESAINVAEGKKQAQILASEAEKAEQINQAAGEASAVLAKAKAKAEAIRILAAALT
   segtresainvaegkkqaqilaseaekaeqinqaageasavlakakakaeairilaaalt
   FRERESLNASIVDAINQAADCWGIRCLRYEIKDIHVPPRVKESMQMQVEAERRKRATVLE
  frereslnasivdainqaadcwgirclryeikdihvpprvkesmqmqveaerrkratvle
   Similarity
  Conservative
   61.2%;
99.7%;
   0;
  Score
Pred.
   Mismatches
  e 218; DB 22;
. No. 4.5e-204;
ismatches 1;
   Length 3007;
  0;
  Gaps
                    326
   266
  86
  206
   206
  0
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  Query Match
Best Local s
Matches 318
   sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of dentifying compounds which bind to polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may have various activities, including cytokine, cell proliferation or cell aliferentiation activities; stem cell growth factor activity; headers of the invention activities; stem cell growth factor activity.
   thrombolytic activities; receptor or ligand activities; or may be involved in oncogenesis, cancer cell proliferation or metastasis. Depending on their biological activities, polypeptides and nucleotides of the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell disorders), chronic inflammatory conditions (e.g., asthma or arthritis), proliferative retinopathy, atherosclerosis, coronary heart disease, arterial ischaemia, bone disorders (e.g., osteoporosis) and abnormal vascular growth. Polypeptides involved with tissue regeneration and repair (or nucleic acids encoding them) may be used to promote wound healing (e.g., of burns, incisions and ulcers), while those with immunomodulatory activities may be used in the treatment of viral, bacterial and fungal infections in addition to immune disorders.
   Polypeptides with growth factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a novel human polypeptide of the invention.
   haematopoiesis regulatory activity; tissue growth activity; immunomodulatory activity; activin- or inhibin-related activities; chemotactic or chemokinetic activities; haemostatic, thrombotic or
  Claim
  e.g. arthritis
  Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject
   03-FEB-2000;
  05-FEB-2001;
   N-PSDB; ABA09225
   27-APR-2000;
  (HYSE-) HYSEQ INC
  Sequence
      109
   49
  87
  27
   2001-457740/49.
318;
  Similarity
  Page 291; 1963pp; English.
  Liu C,
  Conservative
   2000US-0496914.
2000US-0560875.
   2001WO-US03800
  and cancer
  Drmanac
  61.2%;
99.7%;
  0;
  Score 218; DB 22; Pred. No. 6.9e-205;
  Mismatches
  Length 378;
  Indels
  0,:
  Gaps
  0
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AAM79550

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   Дb
   27-APR-2000;
20-JUN-2000;
19-JUL-2000;
01-SEP-2000;
15-SEP-2000;
The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, hammatopoiesis regulating activity, tissue growth factor activity, immnomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
   Human; cytokine; cell proliferation; cell differentiation; gene th vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
  06-NOV-2001
  AAM79550
  Human protein SEQ ID NO 3196
   WPI; 2001-476283/51.
N-PSDB; AAK52683.
   03-FEB-2000;
   05-FEB-2001;
  WO200157190-A2
  Homo sapiens
  Claim
   usetul in
   Nucleic acids encoding polypeptides with
   xue
   Zhao
  20-OCT-2000;
30-NOV-2000;
  (HYSE-)
   349
   169
  327
  289
   σ
   AJ,
  YT,
   TPDSLSSGSSRDVQGTDAS
   frereslnasivdainqaadcwgirclryeikdihvpprvkesmqmqveaerrkratvle
   FRERESLNASIVDAINQAADCWGIRCLRYEIKDIHVPPRVKESMQMQVEAERRKRATVLE
   20; Page 281-282; 6221pp; English
  HYSEQ INC
  standard;
  Yang
  Liu C,
Wang D
Yang Y,
   diagnosis and
   2000US-0654936.
2000US-0663561.
2000US-0693325.
2000US-0728422.
   2000US-0560875.
2000US-0598075.
2000US-0620325.
   2001WO-US04098
  2000US-0496914
  'n
  Wejhrman
  Drmanac RT,
Wang J, Zh
  Protein; 378 AA.
   gene therapy
   345
   Zhang
   Asundi V,
nang J, Ren
   Goodrich
   cytokine-like
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   Zhou
   Chen
   P,
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   Cao
  ZW;
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   therapy;
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RESULT AAB92659
ID AAB92659
ID AC AAB9
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  29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprises at sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprises a sequence complementary to the polynucleotide which comprises a 5'-end sequence where the
  Claim
  Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
   Ota T,
  full-length cDNAs -
  09-JUN-2000;
   28-JUL-2000;
  07-FEB-2001.
   EP1074617-A2
  Homo
  Human; primer;
  Human
   26-JUN-2001
   AAB92659
   AAB92659
  Ishii
   (HELI-)
   147
  147
   327
   327
   267
  267
  207
  207
  87
   87
  27
  ω
   2001-318749/34.
  QHNGDAAASLTVAEQYVSAFSKLAKDSNTILLPSNPGDVTSMVAQAMGVYGALTKAPVPG
  TPDSLSSGSSRDVQGTDAS
   qhngdaaasltvaeqyvsafsklakdsntillpsnpgdvtsmvaqamgvygaltkapvpg
   FRERESLNASIVDAINQAADCWGIRCLRYEIKDIHVPPRVKESMQMQVEAERRKRATVLE
  tpdslssgssrdvqgtdas 345
   rassglprntvvlfvpqqeawvvermgrfhrilepglnilipvldriryvqslkeivinv
  8
  Š
   protein sequence SEQ ID NO:11010
  Isogai T,
  HELIX RES
  SEQ
  standard;
  Sugiyama T,
   99JP-0248036.
99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
   ID 11010;
  2000EP-0116126
   (first entry)
   detection; diagnosis; antisense therapy; gene therapy.
  Nishikawa T,
  Protein;
   2537pp
  Wakamatsu
   345
   +
   CD ROM;
  Ą
  Hayashi K,
  Nagai K,
   English
  Saito
   Saito K,
Otsuki
  ;;
  Yamamoto
  detection by the
   326
  146
  326
   266
  266
  206
  86
   •.
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Homo sapiens antifungal;

vulnerary;

antiulcer

antibacterial;

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RESULT
ABB11981
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  В
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  Matches
  Query Match
Best Local
  bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiinflammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic; cytostatic; osteopathic; vasotropic; cardiant; virucide; antibac
   Human; cytokine; cell proliferation; cell differentiation; growth factor; haematopoiesis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; lymphoid cell disorder; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia;
  oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH13742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; AAB9246 to AAH13632 to AAH13633 can be approximately and AAH13632 to AAH13632 to AAH13632 to AAH13632 to AAH13632 to AAH13632 to AAH13633 can be acid sequences.
  Human SLP-2 homologue, SEQ ID NO:2351.
  11-JAN-2002
   ABB11981 standard; peptide; 378
  Sequence
  of the present invention.
   327
  267
  267
  207
   147
  147
   87
  87
   27
  27
   Local Similarity
  4
   TPDSLSSGSSRDVQGTDAS
  RASSGLPRNTVVLFVPQQEAWVVERMGRFHRILEPGLNILIPVLDRIRYVQSLKEIVINV
   PEQSAVTLDNVTLQIDGYLYLRIMDPYKASYGVEDPEYAVTQLAQTTMRSELGKLSXDKV
  tpdslssgssrdvqgtdas
  freres \verb|lnas| ivdain qaadcwg| irclryeikd| ihvpprvkes mqmqveaerrkratvle
  rassglprntvvlfvpqqeawvvermgrfhrilepglnilipvldriryvqslkeivinv 86
   FRERESLNASIVDAINQAADCWGIRCLRYEIKDIHVPPRVKESMQMQVEAERRKRATVLE
  peqsavtldnvtlqidgvlylrimdpykasygvedpeyavtqlaqttmrselgklsldkv
   318;
   356
   Conservative
   (first entry)
  AA;
   61.2%;
   345
   0;
   Score 218; DB 22;
Pred. No. 6.5e-205;
   Mismatches
  Length 356;
   Indels
  0;
  Gaps
   146
  86
  326
   326
   266
   206
  146
  266
  206
   0
```

```
RESULT AAW78160
ID AAW78160
XX AAW7
XX AAW7
XX AAW7
XX AAW7
XX AWW
AC AAW7
XX Huma
XX Huma
XX Huma
XX Huma
XX Huma
XX Giagg
KW Giagg
KW Giagg
KW Infil
XW Infil
XW Cogn
XX Homo
XX Homo
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  В
   Query Match
Best Local Similarity
  Matches
   Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; lumnune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzhelmer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
   The present sequence represents human integral membrane protein (IMP). IMP may be administered to a subject to treat disorders associated with abnormal ion transport or membrane conductance as well as a variety of tumours, e.g. haemolytic anaemias and prostate, breast and pancreatic tumours. A vector capable of expressing IMP, or a fragment or a derivative thereof, may also be administered to a subject to treat the haemolytic anaemias and prostate, breast and pancreatic tumours.
   Claim
   DNA encoding human integral membrane protein - useful for recombinant protein, for treatment of anaemia and cancer
  Sequence
  Human secreted protein encoded by gene 35 clone HTXCS21.
  13-APR-1999
   AAW78160 standard; Protein;
                                Homo
  241
   121
  301
  301
  241
   181
   181
  121
  61
  61
   N
   MLARAARGHWGPFAEGLSTGFWPRSGRASSGLPRNTVVLFVPQQEAWVVERMGRFHRILE
   NPGDVTSMVAQAMGVYGALTKAPVPGTPDSLSSGSSRDVQGTDASXDEELDRVKMS 356
  HVPPRVKESMQMQVEAERRKRATVLESEGTRESAINVAEGKKQAQILASEAEXAEQINQA
  DPEYAVTQLAQTTMRSELGKLSXDKVFRERESLNASIVDAINQAADCWGIRCLRYEIKDI 180
   PGLNILIPVLDRIRYVQSLKEIVINVPEQSAVTLDNVTLQIDGVLYLRIMDPYKASYGVE
   1998-347418/30
   SK, Hillman JL;
                              sapiens
   dpeyavtqlaqttmrselgklsxdkvfrereslnasivdainqaadcwgirclryeikdi
  AGEASAVLAKAKAKAEAIRILAAALTQHNGDAAASLTVAEQYVSAFSKLAKDSNTILLPS
   hvpprvkesmqmqveaerrkratvlesegtresainvaegkkqaqilaseaekaeqinqa
  pglnilipvldriryvqslkeivinvpeqsavtldnvtlqidgvlylrimdpykasygve
   1; Column
  AAV28867
  356 AA;
  Conservative
  (first entry)
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Pred. No.
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WO9856804-A1.

Qy

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Query Match
Best Local Similarity
Matches 318; Conserv

Conservative

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Mismatches

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Score 218; Pred. No. 6.

DB 20; 5.5e-205;

Length

Indels

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Sequence

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12-SEP-1997;
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12-SEP-1997;
02-OCT-1997;
02-OCT-1997;
02-OCT-1997;
02-OCT-1997;
                                portion (e.g. AAX04302) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to 86 novel genes and their fragments (nucleic acid sequences: AAX04311-X04410; amino'acid sequences AAW78126-W78225) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 86 polynucleotides, based on which tissues they are most highly expressed in the second content of the second content of the 86 polynucleotides.
   New isolated human genes and the secreted polypeptides they encode useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
   This sequence represents a secreted human protein encoded by the gene clone detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Fc
   N-PSDB;
  Yu
   Brewer
  08-JUL-1997
18-AUG-1997
   02-OCT-1997
   11-JUN-1998
   17-DEC-1998
  Claim 11; Page 282-283; 380pp; English.
  12-SEP-1997
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  13-JUN-1997
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   Moore PA,
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  GL;
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                        AAX04311
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Ni J, Olsen
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   GENOME
  97US-0060844.
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  SCI INC
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  Result
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Perfect score:
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  GenCore version Copyright (c) 1993 - 2000
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Human secreted pro
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Novel
Novel
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   cell updates/sec
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| KAE16, amphiphilic | de #13     | Drosophila melanog | Novel human diagno | Drosophila melanog | micum        | #551     | #574 | 6        | bone m   | rain e   | #543     |          | peptide | cancer-as | መ        | İS       | thali    | İS       |          | ŝ        | ö<br>Ö   | is       | is       | S        | S        | Sis      | la m     | of. | o f      | of. | ent of human | Novel human secret |

## ALIGNMENTS

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breast; pancreatic; tumour; ion transport.

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03-AUG-1998 (first entry)

Human integral membrane protein.

AAW57232;

AAW57232 standard; Protein;

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EU Arabidopsis sequencing SEQUENCE FROM N.A.

project

EU Arabidopsis sequencing project; Submitted (MAR-1999) to the EMBL/G

EMBL/GenBank/DDBJ

databases

SEQUENCE FROM N.A.

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RESULT
Q9T082
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   Query Match
Best Local Similarity
Matches 13; Conser
  Bevan M.,
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  Q9T082; PRELIMINARY;
Q9T082; O1-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2001 (TrEMBLrel. 17,
   Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K., Goldsmith A.D., Lee J.M., Quach H.L., Tang C., Toriumi M., Yu G., Bowser L., Carninci P., Chen K., Hayashizaki Y., Ishida Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R., Theologis A., "Full Length cDNA of gene AT4927580 (G1:7269612).";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY059109; AAL15215.1; -. EMBL; AY034924; AAK59431.1; -.
  SEQUENCE FROM N.A.

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Yamada K., Banh J., Banno F., Chang E., Dale J.M., Goldsmith A.D., Yamada K., Dondera C.S., Quach H.L., Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Cheuk Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kin C., Koesema E., Lan B., Lin J., Meyers M.C., Mirands Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tracy S.E., Shinozaki K., Davis R.W., Full Length CDNA of gene AT4927580 (GI:7269612).";

"Full Length CDNA of gene AT4927580 (GI:7269612).";
   Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eueurosids II; Brassicales; Brassicaceae; Arabidopsis.
  HYPOTHETICAL 55.9 KDA PROTEIN. T29A15.70 OR AT4G27580.
  Submitted
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   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
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  153
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Van Der Schueren J., Chuang Y-J., Voet M.,
G., Hoheisel J., Mewes H.W., Mayer K.F.X.,
(MAR-1999) to the EMBL/GenBank/DDBJ databas
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411 AA;
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edons; core eudicots; Rosidae;
  databases
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  Indels
   eudicots; Rosidae;
   Robben J.,
Schueller
  Tracheophyta;
   Wu H.C.,
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   Miranda M.,
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   RX MEDILINE-ZO195005; PubMed-10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen Z.X.,
RA Hannicher G., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelffer B.D.,
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RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Bessley E.M.,
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RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
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RA Mentlov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Harshop D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
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RA Hardshap S.M., Woodage T., Worther E., Wang A.H., Wang X.,
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RA Hardshap S.M., Roodage T
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01-MAY-2000
01-JUN-2001
   Pterygota; Neoptera; Ephydroidea; Drosophi NCBI_TaxID=7227;
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Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

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  IVDAINQAADCWGIRCLRYEIKDIHVPPRVKESMQMQVEAERRKRATVLESEGTRESAIN 216
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(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 17, Last annotation updat
  PRELIMINARY;
   100.0%;
  0;
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  PRT;
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  323
  5.6e-96;
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  update)
  Indels
  Gaps
  0;
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  Matches
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PRINTS; PR00721; STOMATIN.
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Barlow K.
  01-NOV-1999 (TrEMBLrel.
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01-DEC-2001 (TrEMBLrel.
   Q9XVP9;
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01-OCT-2000 (TrEMBLrel.
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InterPro; IPR001107; Band
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Spermatophyta; Magnoliophyta;
  01-OCT-2000 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
STOMATIN-LIKE PROTEIN.
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  investigating biology.";
Science 282:2012-2018(1998).
   SEQUENCE FROM N.A. MEDLINE=99069613;
  Submitted
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Nadimpalli R., Yalpani N.,
                            NCBI_TaxID=4577;
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  Zea mays (Maize)
  STM1.
   STOMATIN-LIKE
   "Genome sequence
  40 FVPQQEAWVVERMGRFHRIL
   Local
   47
   40 FVPQQEAWVVERMG
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   8
   FVPQQEAWVVERMGRFHRIL
   FVPQQEAWVVERMG
   . Similarity 20; Conser
  Similarity 14; Conser
  PROTEIN
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   (OCT-1996)
  Conservative
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  PRELIMINARY;
                                       Andropogoneae;
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  of the
  PubMed=9851916;
   53
   35668 MW;
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  5.6%;
   3.9%;
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   Band_7
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   Streptophyta; Embryophyta; Tracheophyta;
yta; Liliopsida; Poales; Poaceae; PACC cl
   %; Score 14; DB
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  EMBL/GenBank/DDBJ databases
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  0;
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  Created)
  Score 20;
Pred. No.
  PRT;
  Liliopsida;
   D5C6241445FEF4DE CRC64;
   10F98BB9AB44E5ED CRC64;
   Mismatches
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 G.S.,
   .elegans:
  334
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  DB 5; Ld 3.8e-11;
   3.3e-05;
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  Simmons
   DB 5;
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  platform
   Length 323;
  C.R.;
  Length 334;
  PACC clade;
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Q9DCG8
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   AX MEDINE-2049367; PubMed-11042152;

AX Zhang Q.H., Ye M., Wu X.Y., Ren S.X., Zhao M., Zhao C.J., Fu G.,

AX Shen Y., Fan H.Y., Lu G., Zhong M., Xu X.R., Han Z.G., Zhang J.W.,

AX Tao J., Huang Q.H., Zhou J., Hu G.X., Gu J., Chen S.J., Chen Z.;

"Cloning and functional analysis of cDNAs with open reading frames for

"Topolity undefined genes expressed in CD34+ hematopoietic

"Topolity cells.";

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01-JUN-2001 (TrEMBLrel. 1:
0610038F01RIK PROTEIN.
  Q9P042;
Q9P042;
Q1-OCT-2000
Q1-OCT-2000
Q1-DEC-2001
SEQUENCE FROM N.A.

STRAIN-C57BL/6J; TISSUE-KIDNEY;

MEDLINE-2108560; PubMed-11217851;

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda Arakawa T., Izawa M., Nishii K., Kiyosawa H., Kondo S., Yamanaka Alzawa K., Izawa M., Nishii K., Kiyosawa H., Kondo S., Yamanaka Salto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Homo sapiens (Human).
Homo sapiens (Human).
Tharvota; Metazoa; Chordata; Metazoa; Primates;
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  TVLESEGTRESAINVAEGKKQAQILASEAEKAEQINQAAGEASAVLAKAKAKAEAIRILA
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Last sequence update)
Last annotation update)
  Created)
Last sequence update)
Last annotation update)
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Pred. No. 1.7e-132;
   331
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   Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
   7958C0E3BDBE53E5 CRC64;
  Mismatches
   353
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  0;
   Length 342;
  Indels
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  Gaps
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RESULT
Q99JB2
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  STRAIN=FVB; TISSUE=KIDNEY;
Chang J.G., Chan W.L.;
"Mouse stomatin-like protein 2 (MSLP2) mRNA.";
submitted (NOV-2000) to the EMBL/GenBank/DDBJ da'
EMBL; BC003425; AAH03425.1; -
EMBL; BC003425; AAH03425.1; -
EMBL; AF323178; AAG53404.1; -
EMBL; AF323178; AAG53404.1; -
EMBL; AF32131842; 0610038F01Rik.
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InterPro; IPR001972; Stomatin.
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Q99JB2;
Q99JB2;
01-JUN-2001 (TrEMBLTel. 17, C.
01-JUN-2001 (TrEMBLTel. 17, L.
01-DEC-2001 (TrEMBLTel. 19, L.
RIKEN CONA 0610038F01 GENE (S'
   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Unarachianii V.
   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
   "Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001)
EMBL; AK002793; BAB22363.1; -.
MGD; MGI:1913842; 0610038F01Rik.
InterPro; IPR001107; Band_7.
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Query Match

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   Nishikawa T., Nagai K., Suyunc
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| 11         | 15                | 16     | 17          | ъ           | 11          | N           | 16       | 17          | ഗ           | 16          | 16          | N           | 16          | Ŋ           | σ        | 2          | თ          | თ          | ဖ           | ű           | σ          | տ          | ഗ           | 10          | 16          | 16          | 9          | თ          |
| Q9CSJ6     | Q91HW7            | Q92WW3 | 09хвл8      | Q9TXE2      | 088728      | Q939R0      | Q98AP9   | Q9YC53      | Q26834      | Q9ZJ64      | 026072      | Q9APJ7      | Q9I0S4      | Q26830      | Q28882   | Q53840     | Q9VPR0     | Q9NED3     | 080256      | Q18703      | Q9VTX7     | 077238     | 062022      | 004471      | Q9HXE1      | Q9A8D4      | Q94M69     | 077376     |
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| ıs musculu | human immun       |        | aeropyrum p | chlamys nip | mus musculu | fibrobacter |          | aeropyrum p | trypanosoma | helicobacte | helicobacte | hyphomicrob | pseudomonas | trypanosoma | ls aries | polyangium | drosophila | leishmania | vibrio chol | caenorhabdi | drosophila | drosophila | caenorhabdi | arabidopsis | pseudomonas | caulobacter | treptococc | lasmodium  |

## ALIGNMENTS

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Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Craniata; Vertebrata; Euteleostomi;

NCBI\_TaxID=9606;

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RESULT OPPURED TO THE PROPERTY OF THE PROPERTY
  wang Y., Morrow J.S.;
"Identification and Characterization of Human SLP-2, a Novel Homologue of Stomatin (band 7.2b) Present in Erythrocytes and Other Tissues."; Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
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   ADDRESSEE: Harris Brotman STREET: 202 Coast Blvd., Suite 111
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  La Jolla
: California
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US-09-320-774-8

Sequence 8, Application US/09320774

Patent NO. 626545

GENERAL INFORMATION:
APPLICANT: Jarvik, Jonathan W.
TITLE OF INVENTION: READING FRAME
TITLE OF INVENTION: TAGGING
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
   Sequence 2, Application US/08745404B

Patent NO. 6096717

GENERAL INFORMATION:
APPLICANT: Jarvik, Jonathan W.
TITLE OF INVENTION: Method For Producing Tagged Genes,
TITLE OF INVENTION: Transcripts And Proteins
FILE REFERENCE: 2087-961422

CURRENT APPLICATION NUMBER: US/08/745,404B

CURRENT FILING DATE: 1996-11-08

EARLIER APPLICATION NUMBER: 08/000,619

EARLIER APPLICATION NUMBER: 08/000,619

EARLIER APPLICATION TO NOC. 7
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   ; TYPE: PRT
; ORGANISM: Chlamydomonas
US-08-745-404-2
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   밁
  Дb
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   NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 516
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TAGGING
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  441
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ADDRESSEE: STREET: 2

3: Harris Brotman 202 Coast Blvd.,

Suite 111

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  US-08-762-106-9
   TELEPHONE: (619) 654-24:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 516 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
   Sequence 9, Application US/08762106
Patent NO. 5948677
GENERAL INFORMATION:
APPLICANT: Jarvik, Jonathan W.
TITLE OF INVENTION: READING FRAN
TITLE OF INVENTION: TAGGING
  Ouery Match 5.9%; Score 104.5; DB 4; Best Local Similarity 25.6%; Pred. No. 0.067; Matches 74; Conservative 33; Mismatches 95;
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   TELECOMMUNICATION INFORMATION:
   ATTORNEY/AGENT INFORMATION: NAME: Brotman, Harris F.
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APPLICATION NUMBER:
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                      COUNTRY: U
ZIP: 92037
   ADDRESSEE: Harris Brotman
STREET: 202 Coast Blvd., (
CITY: La Jolla
STATE: California
  55 FHRILEPGLNILIPVLDRIR--YVQSLKEIVINVPEQSAVTLDNVTLQIDGVLYLRIMDP 112
   FILING DATE:
CLASSIFICATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
   REGISTRATION NUMBER:
   FILING DATE:
  APPLICATION NUMBER:
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   La Jolla
: California
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   654-2428
   US 08/762,106
  US/09/320,774
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  Suite 111
  FRAME INDEPENDENT EPITOPE
   DB 4; Length 516;
   Indels
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   Gaps
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  US-08-762-106-9
  Sequence 9, Application US/09320774
Patent No. 6265545
GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOETWARE: PatentIn Release #1.0, V.
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/09/320,774
FILING DATE:
  INFORMATION FOR SEQ ID NO:
   NAME: Brotman, Harris F. REGISTRATION NUMBER: 35,461 TELECOMMUNICATION INFORMATION:
   OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
   APPLICANT: Jarvik, Jonathan W.
TITLE OF INVENTION: READING FRAME INDEPENDENT EPITOPE
TITLE OF INVENTION: TAGGING
   MOLECULE TYPE: protein FRAGMENT TYPE: internal
  SEQUENCE CHARACTERISTICS
LENGTH: 527 amino acid
  ATTORNEY/AGENT INFORMATION:
  CORRESPONDENCE ADDRESS
  NUMBER OF SEQUENCES:
   453 -----
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  STREET: 202 Coast
CITY: La Jolla
STATE: California
   COUNTRY: UZIP: 92037
CLASSIFICATION:
  ADDRESSEE:
   55 FHRILEPGLNILIPVLDRIR--YVQSLKEIVINVPEQSAVTLDNVTLQIDGVLYLRIMDP 112
  Match 5.9%;
Local Similarity 25.6%;
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  APPLICATION NUMBER: US/0 FILING DATE: 09-DEC-1996
  TELEPHONE
  CLASSIFICATION:
   MEDIUM TYPE:
   FDRLVSSGY-IYDPVMREVETAFMPWLKEQAIGYLAR------GVVARRVVDK 313
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  E: Harris Brotman
202 Coast Blvd., Suite 111
   SD
  Conservative
   ------LPDGVEPVDVEAEVAKAV---EAVPKPPVKEVTD 483
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   IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
   Floppy disk
  US/08/762,106
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

US 08/762,106

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US-08-745-404-3
  US-09-320-774-9
   GENERAL INFORMATION:
APPLICANT: Jarvik, Jonathan W.
APPLICANT: Jarvik, Jonathan W.
TITLE OF INVENTION: Method For Producing Tagged Genes,
TITLE OF INVENTION: Transcripts and Proteins
FILE REFERENCE: 2087-961422
CURRENT FILING DATE: 1996-11-08
EARLIER APPLICATION NUMBER: 08/000,619
EARLIER FILING DATE: 1993-01-05
EARLIER FILING DATE: 1993-01-05
   NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 654-2428
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  SEQUENCE CHARACTERISTICS:
LENGTH: 527 amino acids
TYPE: amino acid
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  RESULT 15
US-08-216-894-2
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   GENERAL INFORMATION:
APPLICANT: Benichou, Gilles
APPLICANT: Fedoseyeva, Eugenia
APPLICANT: Fedoseyeva, Eugenia
TITLE OF INVENTION: Involvement of Autoantigens in Cardiac
TITLE OF INVENTION: Graft Rejection
  Sequence 2, Application US/08216894 Patent No. 5876734
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SEQ ID NO 1
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               GENERAL INFORMATION:
APPLICANT: Kirchhoff, Louis V.
APPLICANT: Otsu, Keiko
TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION
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CURRENT FILING DATE: 1999-05-12
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MEDIUM TYPE: Floppy disk
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OPERATING SYSTEM: PC-DOS/MS-POS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/216,894
FILING DATE: 24-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 85326/102/DRLO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5309
TELEFAX: 202)672-5309
TELEFAX: 5044136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CARRACTERISTICS:
LENGTH: 564 mmino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: protein
US-08-216-894-2
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Search completed: September 22, 2002, 18:21:40 Job time: 3406 sec
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ADDRESSEE: Foley 6 Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
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   Run on:
  OM protein - protein search, using sw model
  Searched:
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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  3502263
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| No. | 1    | Query<br>Match | Query<br>Match Length DB ID | DB  | ID                   | Description       |
|-----|------|----------------|-----------------------------|-----|----------------------|-------------------|
| Ļ   | 1646 | 93.2           |                             | _ ; | 1 PCT-US98-12125-145 | Sequence 145, App |
| 2   | 1646 | 93.2           | 356                         | 16  | US-09-209-462B-150   | Sequence 150, App |
| ω   | 1646 | 93.2           | 378                         | _   | PCT-US01-03800A-2351 | Sequence 2351, Ap |
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| J   | 1643 | 93.0           | 3007                        | Ь   | PCT-US01-04942A-222  | Sequence 222, App |
| 6   | 1643 | 93.0           | 3019                        | _   | PCT-US01-08656-10594 | Sequence 10594, A |
| 7   | 1635 | 92.5           | 358                         | ٦   | PCT-US01-04098A-1228 | Sequence 1228, Ap |
|     |      |                |                             |     |                      |                   |

| 43 4                               | 47<br>47                               | 38 480<br>39 477<br>40 4                                 | . L UT (                           | ח נח                                                  | 32 619                               | · ~1 ·      | ~                                      | ;              | 79<br>79    |                   | 70                |                   | 20 8              |                  | 89              |                 | 106              | 106              |               | ا سا           | 11 14    | _ د            | 8 14            |
|------------------------------------|----------------------------------------|----------------------------------------------------------|------------------------------------|-------------------------------------------------------|--------------------------------------|-------------|----------------------------------------|----------------|-------------|-------------------|-------------------|-------------------|-------------------|------------------|-----------------|-----------------|------------------|------------------|---------------|----------------|----------|----------------|-----------------|
| 200                                | 5 5 2                                  | 7.5 27.<br>1.5 27.                                       |                                    | л (л<br>а                                             |                                      |             | 16<br>4                                | 16 4           | л.<br>л.сл  |                   | 96<br>4           | 99 4              | 03 4              | 26 4             | .5              | 46 5            | .5 .             | .5<br>6          | 88            | 88             | 800      | 200            | 193 84.         |
|                                    |                                        | 0 320<br>8 316                                           |                                    |                                                       |                                      |             |                                        |                |             |                   |                   |                   |                   |                  |                 |                 |                  |                  |               |                |          |                |                 |
|                                    | NN                                     | 19<br>18                                                 | 122                                | งผะ                                                   | ۰ ۸ ۸                                | N           | N N                                    | N 6            | งผ          | N F               | رم د              | N                 | N 1               | ຸດ               |                 | _               | N                | N                | N             | N I            |          | ــر د          |                 |
| -09-739-449-115<br>-09-803-110-115 | S-09-897-516-7262<br>S-60-215-161-7262 | -60-096-409-1685<br>-09-543-681A-697<br>-09-489-039A-132 | -09-708-427-125<br>-09-248-796-168 | 09-41/-30/-3236<br>09-708-427-5709<br>09-620-3948-403 | S-09-806-866-11<br>S-60-324-109-3211 | -09-806-866 | -09-806-866<br>-09-806-866             | -09-806-866-13 | -09-708-427 | 67-129            | -09-708-427-5669  | S-09-708-427-5669 | -427              | -09-620-394B-403 | -60-167-217-552 | -US01-04942A-59 | S-60-191-637-543 | S-09-614-150-541 | -09-724-497-3 | -09-723-594-36 | 98-733A- | S-09-209-462B- | -US98-12125-272 |
| - 01 01                            | 7262,<br>7262,                         | 1685<br>6978<br>1329                                     | Ψω.                                | 57094,<br>57091                                       | 3211                                 | 17,         | Sequence 19, Appl<br>Sequence 15, Appl | 13,            | 57092,      | Sequence 2, Appli | Sequence 56697, A | 56696,            | Sequence 12342, A | 4030, A          | 5529,           | 598, App        | 5433, A          | 5415             | ω             | ω (            | o 0      | e 411          | 27              |

## ALIGNMENTS

| APPLICATION NUMBER:  APPLICATION NUMBER:  ATTORNEY/AGENT INFORMATION:  NAME: A. Anders Brookes  REGISTRATION NUMBER: 36,373  REFERENCE/DOCKET NUMBER: PZ008Complete | COMPUTER: HP VECTEA 486/33  ODERATING SYSTEM: MSDOS version 6.2  SOFTWARE: ASCII Text  CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US98/12125  FILING DATE: Jan 01, 1900  CLASSIFICATION: | : STREET: 9410 Key West Avenue CITY: Rockville STARE: Maryland COUNTRY: USA ZIP: 20850 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage | PCT-US98-12125-145  Sequence 145, Application PC/TUS9812125  GENERAL INFORMATION: APPLICANT: Rosen et al. TITLE OF INVENTION: 86 Human Secreted Proteins NUMBER OF SEQUENCES: 318 CORRESPONDENCE ADDRESS: ADDRESSEE: Human Genome Sciences, Inc. |
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   PCT-US98-12125-145
   Sequence 150, Application US/09209462B GENERAL INFORMATION:
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Best Local :
  Matches
   TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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FILING DATE: 1997-06-13
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Pred. No. 3.7e-143;
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  118
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; TYPE: PRT
; ORGANISM: Homo s
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   SOFTWARE: P
  Matches
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PRIOR ETLING DATE: 1997-10-02
PRIOR APPLICATION NUMBER: 60/
PRIOR ETLING DATE: 1997-10-02
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   PRIOR
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   APPLICATION NUMBER: FILING DATE: 1997-
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2; Mismatches 11;
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4;

Gaps

2

58

RESULT

356

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RESULT 4
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PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 2700
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LENGTH: 378
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  GENERAL INFORMATION: APPLICANT: Hyseq, I
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  APPLICANT: Hyseq, Inc.
APPLICANT: Tang, Y, Tom et al
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-030
  PRIOR APPLICATION NUMBER: Not Yet Assigned PRIOR FILING DATE: 2001-01-30 PRIOR FILING DATE: 2000-11-30 PRIOR EPILING DATE: 2000-11-30 PRIOR APPLICATION NUMBER: 09/693,325 PRIOR APPLICATION NUMBER: 09/693,325 PRIOR FILING DATE: 2000-10-20 PRIOR APPLICATION NUMBER: 09/663,561 PRIOR APPLICATION NUMBER: 09/663,561 PRIOR APPLICATION NUMBER: 09/663,561 PRIOR EPILING DATE: 2000-09-15
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  299
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   59 LEPGLNILIPVLDRIRYVQSLKEIVINVPEQSAVTLDNVTLQIDGVLYLRIMDPYKASYG 118
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FILING DATE: 2000-09-15
APPLICATION NUMBER: 09/654,936
FILING DATE: 2000-09-01
APPLICATION NUMBER: 09/620,325 FILING DATE: 2000-07-19
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Pred. No. 4.1e-143;
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   Indels
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  Gaps
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ORGANISM: Homo sapiens PCT-US01-04942A-222
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Score

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DB

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356

298 298 238 238

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PRIOR APPLICATION NUMBER: 09/770,160
PRIOR FILING DATE: 2001-01-26
NUMBER OF SEO ID NOS: 10994
SOFTMARE: CUStom
SEO ID NO 10594
LENGTH: 3019
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   RESULT 6
PCT-US01-08656-10594
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Matches 340
  GENERAL INFORMATION:
APPLICANT: HYSEG, Inc
TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC
FILE REFERENCE: 21272-066
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  AND POLYPEPTIDES
  Indels
  4
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  Gaps
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  298
                      118
  oy eMATRIX, score of 16.91
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PRIOR FILING DATE: 2000-09-01
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   QAAGEASAVLAKAKAEAIRILAAALTQHNGDAAASLTVAEQYVSAFSKLAKDSNTILL
  DIHVPPRVKESMQMQVEAERRKRATVLESEGTRESAINVAEGKKQAQILASEAEKAEQIN
   VEDPEYAVTQLAQTTMRSELGKLSLDKVFRERESLNASIVDAINQAADCWGIRCLRYEIK
  LEPGLNILIPVLDRIRYVQSLKEIVINVPEQSAVTLDNVTLQIDGVLYLRIMDPYKASYG
  MLARAARGTGALLLRGSLLASGRAPR - - RASSGLPRNTVVLFVPQQEAWVVERMGRFHRI
  PSNPGDVTSMVAQAMGVYGALTKAPVPGTPDSLSSGSSRDVQGTDASLDEELDRVKMT
   VEDPEYAVTQLAQTTMRSELGKLSXDKVFRERESLNASIVDAINQAADCWGIRCLRYEIK 178
   LEPGLNILIPVLDRIRYVQSLKEIVINVPEQSAVTLDNVTLQIDGVLYLRIMDPYKASYG
 Conservative
   Novel Nucleic Acids and Polypeptides
  92.5%;
   2;
   Score 1635; DB 1;
Pred. No. 3.9e-142;
2; Mismatches 11;
  Length
   Indels
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Gaps

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118 118

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   PCT-US98-12125-272 ; Sequence 272, Application PC/TUS9812125
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  PCT-US98-12125-272
  Matches 304;
   Query Match
   TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
  GENERAL INFORMATION:
   REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PZ008Complete
TELECOMMUNICATION INFORMATION:
  SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC'
FILING DATE: Jan 01, 1
   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
   COMPUTER READABLE FORM:
  CORRESPONDENCE ADDRESS
   APPLICANT: Rosen et al.
TITLE OF INVENTION: 86 Human Secreted Proteins
NUMBER OF SEQUENCES: 318
  APPLICANT:
  ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
   111 DPYKASYGVEDPEYAVTQLAQTTMRSELGKLSXDKVFRERESLNASIVDAINQAADCWGI 170
  299
   239
  239 QAAGEASAVLAKAKAKAEAIRILAAALTQHNGDAAASLTVAEQYVSAFSKLAKDSNTILL
  179
    291
                                  181
   121
  MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2
  TYPE: amino acid
  51 RMGRFHRILEPGLNILIPVLDRIRYVQSLKEIVINVPEQSAVTLDNVTLQIDGVLYLRIM 110
  Local Similarity
   COUNTRY:
   STATE:
  TELEPHONE:
  FILING DATE:
   STREET:
  ADDRESSEE:
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   PSNPGDVTSMVAQAMGVYGALTKA--PVPGTPDSLSSGSSRDVQGTDASXDEELDRVKMS 356
  KDSNTILLPSNPGDVTSMVAQAMGVYGALTKAPVPGTPDSLSSGSSRDVQGTDASXDEEL 350
   AEKAEQINQAAGEASAVLAKAKAKAEAIRILAAALTOHNGDAAASLTVAEQYVSAFSKLA 290
  QAAGEASAVLAKAKAEAIRILAAALTQHNGDAAASLTVAEQYVSAFSKLAKDSNTILL
  DIHVPPRVKESMQMQVEAERRKRATVLESEGTRESAINVAEGKKQAQILASEAEKAEQIN
                               AEKAEQINQAAGEASAVLAKAKAKAEAIRILAAALTQHNGDAAASLTVAEQYVSAFSKLA
   RMGRFHRILEPGLNILIPVLDRIRYVQSLKEIVINVPEQSAVTLDNVTLQIDGVLYLRIM 60
   20850
  Rockville
   Maryland
   E: Human Genome Sciences, Inc
9410 Key West Avenue
   306 amino acids
  Conservative
   USA
  (301)
   Jan 01, 1900
   84.5%;
  309-8504
   PCT/US98/12125
  272:
  0;
  Score 1493; DB 1;
Pred. No. 4.3e-129;
0; Mismatches 2;
  Length 306;
  Indels
  0;
  Gaps
   298
                                240
   298
  238
  0;
```

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   RESULT 9
US-09-209-462B-411
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   Вр
   GENERAL INFORMATION:
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   PRIOR FILING DATE: 1997-UD-13
PRIOR APPLICATION NUMBER: 60/(
PRIOR APPLICATION NUMBER: 1997-06-13
  APPLICANT:
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PRIOR
  PRIOR FILING DATE: 1997-06-13
PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1997-06-13
PRIOR APPLICATION NUMBER: 60/
PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1997-06-13
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PRIOR FILING DATE: 1997-09-12
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PRIOR FILING DATE: 1997-06-13
  PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1997-
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  PRIOR APPLICATION NUMBER:
   PRIOR FILING DATE:
   301
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   FILING DATE: 1997-10-02
APPLICATION NUMBER: 60/C
APPLICATION NUMBER: 60/C
  APPLICATION NUMBER: FILING DATE: 1997-0
   APPLICATION NUMBER: FILING DATE: 1997-APPLICATION NUMBER:
  APPLICATION NUMBER: 60/
FILING DATE: 1997-09-12
   APPLICATION NUMBER: 60/
FILING DATE: 1997-09-12
APPLICATION NUMBER: 60/
   FILING DATE: 1997-0
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  APPLICATION NUMBER: 60/
FILING DATE: 1997-06-13
  APPLICATION NUMBER: FILING DATE: 1997-0
   APPLICATION NUMBER: 60/
FILING DATE: 1997-06-13
  FILING DATE:
  APPLICATION NUMBER:
   APPLICATION NUMBER: 60/
FILING DATE: 1997-10-02
  FILING DATE:
   APPLICATION NUMBER:
  APPLICATION NUMBER:
            FILING DATE:
                            APPLICATION NUMBER:
   FILING DATE:
  FILING DATE:
   APPLICATION NUMBER:
  APPLICATION NUMBER:
  DRVKMS 306
   DRVKMS 356
   Rosen et al.
PENTION: 86 Human Secreted Proteins
   Application US/09209462B
  PZ008P1
                                       1997-10-02
  омвек: 60/050,901
1997-06-13
  1997-06-13
   омивек: 60/058,972
1997-09-12
   1997-06-13
   1997-09-12
  1997-08-18
  1997-06-13
            1997-10-02
   1997-07-08
   1997-06-13
   1998-06-11
   1997-09-
  60/058,665
)9-12
   60/049,548
   60/049,549
60/061,059
   60/058,975
   60/058,971
   60/058,750
   60/058,668
  60/055,984
   60/052,989
  60/049,610
  60/049,609
   60/049,608
   60/049,606
   60/049,566
   60/049,550
  60/049,547
   PCT/US98/12125
                           60/060,865
   60/060,844
   60/060,841
   60/060,834
  60/058,669
  60/051,919
   60/049,611
  60/049,607
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PRIOR APPLICATION NUMBER: 60/061,060
PRIOR FILING DATE: 1997-10-02
NUMBER OF SEQ ID NOS: 737
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 411
LENGTH: 306
TYPE: PRT
ORGANISM: Homo sapiens
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   US-09-209-462B-411
  US-09-298-733-36
   CURRENT APPLICATION NUMBER: US/09/298,733
CURRENT FILING DATE: 1999-04-23
EARLIER APPLICATION NUMBER: 60/082,961
EARLIER FILING DATE: 1998-04-24
EARLIER FILING DATE: 1998-05-22
EARLIER FILING DATE: 1998-05-22
EARLIER FILING DATE: 1998-06-11
EARLIER FILING DATE: 1998-06-11
EARLIER FILING DATE: 1998-06-12
EARLIER APPLICATION NUMBER: 60/091,163
EARLIER APPLICATION NUMBER: 60/091,619
EARLIER FILING DATE: 1998-07-02
EARLIER FILING DATE: 1998-07-02
  APPLICANT: Hoffman, Heidi
APPLICANT: Hall, Jeff
APPLICANT: Rapiejko, Peter
APPLICANT: Adams, R. Mark
APPLICANT: Agostino, Michael J.
APPLICANT: Fechtel, Kim
APPLICANT: Howes, Steve H.
   Sequence 36, Application US/09298733 GENERAL INFORMATION:
    NUMBER OF SEQ ID NOS: 79
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 36
LENGTH: 305
  Matches
   Query Match 84.5%;
Best Local Similarity 99.3%;
  TITLE OF INVENTION: Secreted Proteins and TITLE OF INVENTION: Encoding Them FILE REFERENCE: AG199-02pM
   APPLICANT: Valenzuela, Dario
APPLICANT: Yuan, Olive
TYPE: PRI
  181
  111 DPYKASYGVEDPEYAVTQLAQTTMRSELGKLSXDKVFRERESLNASIVDAINQAADCWGI 170
   351 DRVKMS 356
   241
  231
  301 DRVKMS 306
   61
  51 RMGRFHRILEPGLNILIPVLDRIRYVQSLKEIVINVPEQSAVTLDNVTLQIDGVLYLRIM 110
   1 RMGRFHRILEPGLNILIPVLDRIRYVQSLKEIVINVPEQSAVTLDNVTLQIDGVLYLRIM 60
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   KDSNTILLPSNPGDVTSMVAQAMGVYGALTKAPVPGTPDSLSSGSSRDVQGTDASLDEEL
  AEKAEQINQAAGEASAYLAKAKAKAEAIRILAAALTQHNGDAAASLTVAEQYVSAFSKLA 290
   DPYKASYGVEDPEYAVTQLAQTTMRSELGKLSLDKVFRERESLNASIVDAINQAADCWGI 120
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  304; Conservative
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   Score 1493; DB 16;
Pred. No. 4 3e-129;
  Mismatches
  Polynucleotides
  <u>ب</u>
  Length
  Indels
  0;
  Gaps
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  0;
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```
; SEQ ID NO 36
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-298-733A-36
   APPLICANT: Raplejko, Peter
TITLE OF INVENTION: Secreted Proteins and Polynucleotides
TITLE OF INVENTION: Secreted Proteins and Polynucleotides
TITLE OF INVENTION: Encoding Them
FILE REFERENCE: 1966.1009-000
CURRENT APPLICATION NUMBER: US/09/298,733A
CURRENT FILING DATE: 1999-04-23
PRIOR APPLICATION NUMBER: 60/082,961
PRIOR FILING DATE: 1998-04-24
PRIOR FILING DATE: 1998-04-24
PRIOR FILING DATE: 1998-05-22
PRIOR FILING DATE: 1998-06-01
PRIOR APPLICATION NUMBER: 60/089,94
PRIOR APPLICATION NUMBER: 60/089,163
PRIOR FILING DATE: 1998-06-12
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089,163
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089,163
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   ; ORGANISM: Homo sapiens US-09-298-733-36
  US-09-298-733A-36
   Sequence 36, Application US/09298733A
GENERAL INFORMATION:
APPLICANT: Valenzuela, Dario
APPLICANT: Yuan, Olive
APPLICANT: Hoffmann, Heidi
APPLICANT: Hall, Jeff
APPLICANT: Rapiejko, Peter
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Best Local Similarity
Matches 303; Conserv
   Query Match
Best Local Similarity
Matches 303; Conserv
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  292
   181
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  172 CLRYEIKDIHVPPRVKESMOMQVEAERRKRATVLESEGTRESAINVAEGKKQAQILASEA 231
  112
  301 RVKMS 305
61 PYKASYGVEDPEYAVTQLAQTTMRSELGKLSLDKVFRERESLNASIVDAINQAADCWGIR
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   PYKASYGVEDPEYAVTQLAQTTMRSELGKLSXDKVFRERESLNASIVDAINQAADCWGIR 171
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ilarity 99.3%;
Conservative
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Pred. No. 1.2e-128;
O; Mismatches 2;
   Score 1488; DB 16;
Pred. No. 1.2e-128;
   Mismatches
  DB 16;
  Length
   Indels
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  Length 305;
   0;
   0
   Gaps
   Gaps
   240
   180
   120
  351
   0:
   0
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  ; ORGANISM: Homo sapiens
US-09-723-594-36
   CURRENT APPLICATION NUMBER: US/09/723,594
CURRENT FILING DATE: 2000-11-28
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PRIOR FILING DATE: 1999-04-23
PRIOR FILING DATE: 1999-04-23
PRIOR FILING DATE: 1998-04-24
PRIOR PRIOR APPLICATION NUMBER: 60/086,402
PRIOR APPLICATION NUMBER: 60/086,904
PRIOR APPLICATION NUMBER: 60/088,994
PRIOR FILING DATE: 1998-05-22
PRIOR FILING DATE: 1998-06-01
PRIOR APPLICATION NUMBER: 60/089,163
PRIOR APPLICATION NUMBER: 60/091,619
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PRIOR APPLICATION NUMBER: 60/091,619
PRIOR APPLICATION NUMBER: 60/091,619
PRIOR APPLICATION NUMBER: 60/091,619
PRIOR APPLICATION NUMBER: 60/091,619
PRIOR FILING DATE: 1998-06-02
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US-09-723-594-36
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  Sequence 36, Application US/09723594 GENERAL INFORMATION:
   Query Match
Best Local Similarity
Matches 303; Conserv
   SOFTWARE:
   APPLICANT: Valenzuela, Dario B.
APPLICANT: Yuan, Olive
APPLICANT: Hoffmann, Heidi
APPLICANT: Hall, Jeff
APPLICANT: Rapiejko, Peter
TITLE OF INVENTION: Secreted Proteins and Polynucleotides
TITLE OF INVENTION: Encoding Them
FILE REFERENCE: 1966,1009-002
  NUMBER OF SEQ ID NOS:
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TYPE: PRT
  181
  121
 121
  112
   112
   301 RVKMS 305
  61
   61
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   CLRYEIKDIHVPPRVKESMQMQVEAERRKRATVLESEGTRESAINVAEGKKGAQILASEA 231
  RVKMS 356
CLRYEIKDIHVPPRVKESMQMQVEAERRKRATVLESEGTRESAINVAEGKKQAQILASEA
  FastSEQ
  Conservative
  for Windows Version
  84.2%; Score 1488; DB 21; 99.3%; Pred. No. 1.2e-128; 9.3%; O: Mismatches 2;
   Length
   0.
   Gaps
   291
  231
   120
  171
  240
  180
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  ; TYPE: PRT; ORGANISM: Homo sapiens US-09-724-497-36
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  Дb
  δÃ
  Db
   QΥ
   US-09-724-497-36
  PRIOR APPLICATION NUMBER: 60/08
PRIOR FILING DATE: 1998-06-01
PRIOR APPLICATION NUMBER: 60/08
PRIOR FILING DATE: 1998-06-12
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PRIOR FILING DATE: 1998-07-02
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APPLICANT:
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APPLICANT:
  APPLICANT: Rapiejko, Peter
TITLE OF INVENTION: Secreted Proteins and
TITLE OF INVENTION: Encoding Them
FILE REFERENCE: 1966.1009-001
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PRIOR FILING DATE: 1998-05-22
   181
  172 CLRYEIKDIHVPPRVKESMQMQVEAERRKRATVLESEGTRESAINVAEGKKQAQILASEA 231
  241
   181
                                 241
  121
  112 PYKASYGVEDPEYAVTQLAQTTMRSELGKLSXDKVFRERESLNASIVDAINQAADCWGIR 171
   301 RVKMS
  61 PYKASYGVEDPEYAVTQLAQTTMRSELGKLSLDKVFRERESLNASIVDAINQAADCWGIR
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  DSNTILLPSNPGDVTSMVAQAMGVYGALTKAPVPGTPDSLSSGSSRDVQGTDASXDEELD 351
  CLRYEIKDIHVPPRVKESMQMQVEAERRKRATVLESEGTRESAINVAEGKKQAQILASEA
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   EKAEQINQAAGEASAVLAKAKAEAIRILAAALTQHNGDAAASLTVAEQYVSAFSKLAK
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RVKMS
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  Valenzuela, Dario
   Hoffmann, Heidi
Hall, Jeff
  Yuan, Olive
   356
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  84.2%;
   60/089,163
)6-12
  60/088,994
  60/082,961
   60/091,619
  60/086,402
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   Polynucleotides
   DB 21;
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  180
  120
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301 RVKMS

305

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PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR FILING DATE: 1999-10-19
PRIOR PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR APPLICATION NUMBER: 60/173,383
PRIOR APPLICATION NUMBER: 60/173,383
PRIOR FILING DATE: 1999-12-28
PRIOR FILING DATE: 1999-12-28
PRIOR FILING DATE: 1990-12-28
PRIOR FILING DATE: 1990-10-12
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR APPLICATION NUMBER: 60/174,831
PRIOR APPLICATION NUMBER: 60/184,831
PRIOR APPLICATION NUMBER: 60/184,831
              RESULT 15
US-60-191-637-5433
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  S
   ; ORGANISM: DROSOPHILA US-09-614-150-5415
   RESULT 14
US-09-614-150-5415
  PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 60/191,637
PRIOR FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 5415
  Query Match
Best Local Similarity
Matches 209; Conserva
   GENERAL INFORMATION:
  Sequence 5415, Application US/09614150
Sequence 5433, Application US/60191637
  APPLICANT: Venter, J. Craig
APPLICANT: et al.
TITLE OF INVENTION: DETECTION KIT, SUCH AS
TITLE OF INVENTION: ARRAYS, FOR DETECTING
TITLE OF INVENTION: DROSOPHILA GENES.
  FILE REFERENCE: CL000728
   TYPE: PRT
   LENGTH: 323
   219
  241
  279
   121
  294
  181
   159
   61
   99
  39
   L
  VQGTDA-----SXDEELDRVKMS 356
  AEQYIGAFKKLAKTNUTMILPSNPGDVNGFVAQALAVYNHVSNS----
  AEQYVSAFSKLAKDSNTILLPSNPGDVTSMVAQAMGVYGALTKAPVPGTPDSLSSGSSRD 338
   EGKRKSRILASEAERQEHINKASGEAAAIIAVADARARSLLAIAKSLSHLDGQNAASLTL 240
   EGKKQAQILASEAEKAEQINQAAGEASAVLAKAKAKAEAIRILAAALTQHNGDAAASLTV 278
   DSINKASEAWGIACLRYEIRDIRLPTRVHEAMQMQVEAERRKRAAILESEGVREAEINIA 180
  DAINQAADCWGIRCLRYEIKDIHVPPRVKESMOMOVEAERRKRATVLESEGTRESAINVA 218
  VKGVGACLNAKSVEYKELQEDKSSVKMN 321
  Conservative
  60.2%; Score 1064.5; DB 20; 63.7%; Pred. No. 2.1e-89; tive 55; Mismatches 47; Ir
   EXPRESSION OF
  47; Indels
  Length
   10,000
  NOATKSSEN 293
  323;
   ဓ္က
  Gaps
  2
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Search completed: September 22, Job time: 728 sec

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; ORGANISM: DROSOPHILA US-60-191-637-5433
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   GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
TITLE OF INVENTION: NUCLEIC ACID DETECTION KITS COMPRISING
TITLE OF INVENTION: GENE SEQUENCES EXPRESSED FROM THE DROSOPHILA GENOME, AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CLO00392
CURRENT APPLICATION NUMBER: US/60/191,637
CURRENT APPLICATION NUMBER: US/60/191,637
CURRENT FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 42660
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5433
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TYPE: PRT
  Query Match
Best Local
  Matches
   181
   241
   219
   61
  99
  Local Similarity
les 209; Conserv
  AEQYVSAFSKLAKDSNTILLPSNPGDVTSMVAQAMGVYGALTKAPVPGTPDSLSSGSSRD 338
  LQIDGVLYLRIMDPYKASYGVEDPEYAVTQLAQTTMRSELGKLSXDKVFRERESLNASIV 158
                             VQGTDA-----SXDEELDRVKMS 356
VKGVGACLNAKSVEYKELQEDKSSVKMN
   AEQYIGAFKKLAKTNNTMILPSNPGDVNGFVAQALAVYNHVSNS-----
   Conservative
   60.2%;
63.7%;
  ; Score 1064.5; DB 26; Pred. No. 2.1e-89; 55; Mismatches 47;
    321
  DB 26; Length
   Indels
   -- NQATKSSEN
   17;
   323;
  Gaps
  60
  98
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